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Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
							GALECTIN-3 (GALACTOSE-SPECIFIC LECTIN 3) (MAC-2 ANTIGEN) (IGE-BINDING PROTEIN) (35 KD LECTIN) (CARBOHYDRATE BINDING PROTEIN 35) (CBP 35) (LAMININ-BINDING PROTEIN) (LECTIN L-29) (CBP30)
8652	18541	28825	3.94	3.3E-01	P47953	SWISSPROT	
8956	18763		4.79	3.3E-01	AA806621.1	EST_HUMAN	ob71g02.s1 NCL_CGAP_GOB1 Homo sapiens cDNA clone IMAGE:1368850 3'
8972	10000	19791	1.88	3.3E-01	X07990.1	NT	Rhizobium leguminosarum sym plasmid pRL5Jl nodX gene
9119	18881	28789	1.63	3.3E-01	6508319	NT	Homo sapiens aldehyde oxidase 1 (AOX1), mRNA
9817	19823		6.05	3.3E-01	AF000002.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 287001-544000 nt. position (217)
449	10393		1.98	3.2E-01	AF018261.1	NT	Rattus norvegicus EH domain binding protein Epsin mRNA, complete cds
701	10634		2.05	3.2E-01	AL161581.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 61
1146	11059	20902	18.99	3.2E-01	AF047013.1	NT	Fusarium poae virus 1 RNA2 putative RNA dependent RNA polymerase gene, complete cds
1261	11168	21019	1.04	3.2E-01	Z50202.1	NT	P. vulgaris arc5-1 gene
1368	11274	21130	6.25	3.2E-01	Q48624	SWISSPROT	LACTOSE PERMEASE (LACTOSE-PROTON SYMPORT) (LACTOSE TRANSPORT PROTEIN)
1737	11638	21506	1.22	3.2E-01	Z36041.1	NT	S. cerevisiae chromosome II reading frame ORF YBR172c
1744	11645	21513	5.5	3.2E-01	AW957194.1	EST_HUMAN	EST369264 MAGC resequences, MAGD Homo sapiens cDNA
1744	11645	21514	5.5	3.2E-01	AW957194.1	EST_HUMAN	EST369264 MAGC resequences, MAGD Homo sapiens cDNA
1800	11698	21574	1.16	3.2E-01	AL111685.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
2114	12003	21901	2.89	3.2E-01	BF203817.1	EST_HUMAN	601868804F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4111512 5'
2494	12368		2.9	3.2E-01	7710079	NT	Mus musculus Pbx/knotted 1 homeobox (Pknxt1), mRNA
2677	12542	22433	1.55	3.2E-01	AF060588.1	NT	Homo sapiens promyelocytic leukemia zinc finger protein (PLZF) gene, complete cds
3556	13470		0.96	3.2E-01	D10872.1	NT	Humam h NAT allele 3-2 gene for arylamine N-acetyltransferase
3868	13779		0.97	3.2E-01	AL161546.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 46
4295	14193	23977	1.35	3.2E-01	M18818.1	NT	Rabbit beta-like globin gene cluster encoding the epsilon, gamma, delta (pseudogene) and beta globin polypeptides, complete cds
4375	14271	24052	0.81	3.2E-01	AF111167.2	NT	Homo sapiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
4397	14293	24077	1.33	3.2E-01	Q10268	SWISSPROT	HYPOTHETICAL 81.7 KD PROTEIN C13G7.04C IN CHROMOSOME I PRECURSOR
4632	14520		5.86	3.2E-01	BF693617.1	EST_HUMAN	602081972F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4246505 5'
4907	15081		1.18	3.2E-01	M32352.1	NT	Mouse retin (Ret-1-d) gene, complete cds
5133	15000	24771	0.98	3.2E-01	AY008847.1	NT	Homo sapiens interleukin 12 p40 subunit (IL12B) gene, IL12B-1 allele, complete cds
5223	15146	24913	2.82	3.2E-01	BE173964.1	EST_HUMAN	CNV0-HT0569-000300-269-f10 HT0569 Homo sapiens cDNA
6752	16631	26819	1.42	3.2E-01	M60266.1	NT	Rat ISO-atrial natriuretic factor gene, complete cds
6872	16751	26946	13.32	3.2E-01	X02508.1	NT	H. sapiens gene fragment for acetylcholine receptor (AChR) alpha subunit exons 8, 9 and 3' flanking region
6875	16754	26951	14.29	3.2E-01	BF311635.1	EST_HUMAN	601897107F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4126633 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6929	16807		1.35	3.2E-01	AL161574.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 70
6986	16863	27056	1.5	3.2E-01	AE002015.1	NT	Deinococcus radiodurans R1 section 152 of the complete chromosome 1
7247	17124		2.19	3.2E-01	M86511.1	NT	Human monocyte antigen CD14 (CD14) mRNA, complete cds
7741	17591	27812	3	3.2E-01	U44914.1	NT	Borrelia burgdorferi plasmid op32-2, erpC and erpD genes, complete cds; and unknown genes
7910	17760		3.25	3.2E-01	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
8058	17949	28199	2.7	3.2E-01	T06813.1	EST_HUMAN	EST04702 Fetal brain, Stratagene (cat#36206) Homo sapiens cDNA clone HFB221
9152	19662		3.28	3.2E-01	L07288.1	NT	Drosophila melanogaster laminin A (Lam-A) mRNA, complete cds
9669	19228		2.97	3.2E-01	O83217	SWISSPROT	ELONGATION FACTOR TU (EF-TU)
9801	19313		1.58	3.2E-01	L39874.1	NT	Homo sapiens deoxycytidylate deaminase gene, complete cds
9855	19896	24898	1.57	3.2E-01	BE385776.1	EST_HUMAN	601275480F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3616746 5'
2636	12503	22397	3.73	3.1E-01	R18051.1	EST_HUMAN	yes0106.r1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:125051 5' similar to gb:M64241 QM PROTEIN (HUMAN);
2665	12655	22419	3.45	3.1E-01	7661971	NT	Homo sapiens KIAA0174 gene product (KIAA0174), mRNA
2665	12655	22420	3.45	3.1E-01	7661971	NT	Homo sapiens KIAA0174 gene product (KIAA0174), mRNA
2827	12756		1.01	3.1E-01	AW629036.1	EST_HUMAN	hi46108.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2975391 3'
3136	13061		2.78	3.1E-01	AB029089.1	NT	Mus musculus gene for Ser/Thr kinase KIAA0174, exon 6
3832	13744	23536	1.15	3.1E-01	AJ251586.1	NT	Daucus carota mRNA for transcription factor E2F (E2F gene)
5073	14943	24717	0.99	3.1E-01	AA576308.1	EST_HUMAN	nm61h05.s1 NCI CGAP_Br3 Homo sapiens cDNA clone IMAGE:1072761 3'
5365	15285	25119	8.66	3.1E-01	AF178111.1	NT	Homo sapiens hepatocyte nuclear factor-3 alpha (HNF3A) gene, exon 1
5447	15368		45.03	3.1E-01	Y13278.1	NT	Mus musculus mRNA for polycystin
5527	15444	25510	1.94	3.1E-01	AF184122.1	NT	Homo sapiens filamin 2 (FLN2) gene, exons 10 through 22
5890	15796	25918	1.34	3.1E-01	AW983549.1	EST_HUMAN	RC3-HN0001-310300-011-b04 HN0001 Homo sapiens cDNA
6160	19438	24861	2.4	3.1E-01	BE737392.1	EST_HUMAN	601308121F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3640420 5'
7023	16900	27092	1.87	3.1E-01	R45318.1	EST_HUMAN	yg46701.s1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:35639 3'
7791	17641	27874	7.76	3.1E-01	BF696639.1	EST_HUMAN	602124743F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4281611 5'
7791	17641	27875	7.76	3.1E-01	BF696639.1	EST_HUMAN	602124743F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4281611 5'
7832	17682	27926	1.96	3.1E-01	AI244001.1	EST_HUMAN	q161e11.x1 NCI CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1663980 3' similar to gb:S55700 HYDROXYMETHYLGLUTARYL-COA LYASE PRECURSOR (HUMAN);
8211	18095	28348	1.95	3.1E-01	BF216117.1	EST_HUMAN	601883592F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4095814 5'
8823	18636	28920	1.99	3.1E-01	7662291	NT	Homo sapiens KIAA0764 gene product (KIAA0764), mRNA
9279	18982		1.63	3.1E-01	AF294308.1	NT	Anolis opalinus isolate QS NADH dehydrogenase subunit 2 (ND2) gene, complete cds; mitochondrial gene for mitochondrial product
9315	19007		1.64	3.1E-01	AF304182.1	NT	Stizostedion vitreum 40S ribosomal protein S11 mRNA, partial cds
9457	19089		2.45	3.1E-01	AF195953.1	NT	Homo sapiens membrane-bound aminopeptidase P (XNPEP2) gene, complete cds

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9806	19318		3.11	3.1E-01	AF196778.1	NT	Homo sapiens transcription factor (CHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel a>
66	12635	19866	1.58	3.0E-01	6755083	NT	Mus musculus protein kinase C, epsilon (Pkee), mRNA
254	10220	20037	11.12	3.0E-01	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
1204	11114	20960	1.89	3.0E-01	AW300400.1	EST_HUMAN	xs63f08.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2774343 3'
1491	11396	21256	6.26	3.0E-01	AJ006755.1	NT	Balaenoptera physalus gene encoding atrial natriuretic peptide
2089	11978	21873	0.86	3.0E-01	AF237778.1	NT	Rattus norvegicus Ca2+/calmodulin-dependent protein kinase II, alpha subunit mRNA, 3' untranslated region
3175	13100		0.98	3.0E-01	AB030481.1	NT	Corynebacterium sp. ALY-1 alyPG gene for polyglutamate lyase, complete cds
3789	13701	23488	1.34	3.0E-01	AW817785.1	EST_HUMAN	PM1-ST0262-261199-001-g01 ST0262 Homo sapiens cDNA
4412	14306	24089	1.91	3.0E-01	AJ006755.1	NT	Balaenoptera physalus gene encoding atrial natriuretic peptide
5283	15205	24981	5.34	3.0E-01	BE741629.1	EST_HUMAN	601594960F1 NIH_MGC 9 Homo sapiens cDNA clone IMAGE:3948734 5'
5379	15298	25147	3.18	3.0E-01	BE693575.1	EST_HUMAN	RC3-BT0333-180700-111-a03 BT0333 Homo sapiens cDNA
5379	15298	25148	3.18	3.0E-01	BE693575.1	EST_HUMAN	RC3-BT0333-180700-111-a03 BT0333 Homo sapiens cDNA
5401	15320	25368	3.51	3.0E-01	U01247.1	NT	Mus musculus 129/sv Clara cell 10 kd protein (mCC10) gene, complete cds
6086	16031	26171	2.61	3.0E-01	D16313.1	NT	Mouse cytokeratin 15 gene, complete cds
6335	16198	26358	2.57	3.0E-01	10947007	NT	Mus musculus midholin (Midn-pending), mRNA
6429	16290	26451	1.35	3.0E-01	AF071810.1	NT	Streptococcus pneumoniae strain DBL5 PspA (pspA) gene, partial cds
6625	16605	26693	1.25	3.0E-01	AE001755.1	NT	Thermotoga maritima section 67 of 136 of the complete genome
6877	16756		4.67	3.0E-01	9910161	NT	Mus musculus C-type (calcium dependent, carbohydrate recognition domain) lectin, superfamily member 9 (Clec5f9), mRNA
6937	16815	27007	1.27	3.0E-01	BE566083.1	EST_HUMAN	601339079F1 NIH_MGC 53 Homo sapiens cDNA clone IMAGE:3681594 5'
7944	17794	28034	1.89	3.0E-01	AB030231.1	NT	Aspergillus oryzae bpa gene for ER chaperone BIP, complete cds
8980	18785	29074	2.89	3.0E-01	H51029.1	EST_HUMAN	yp84b10.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:194107 5'
8980	18785	29075	2.89	3.0E-01	H51029.1	EST_HUMAN	yp84b10.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:194107 5'
9564	19647		1.43	3.0E-01	AJ297631.1	NT	Rattus norvegicus mRNA for glyceraldehyde-3-phosphate dehydrogenase type 2 (gapdh-2 gene)
9836	19690		2.76	3.0E-01	6677768	NT	Mus musculus ribose 5-phosphate isomerase A (Rpia), mRNA
1978	11871	21762	1.6	2.9E-01	AE000736.1	NT	Aquifex aeolicus section 68 of 109 of the complete genome
2201	12088	21989	0.99	2.9E-01	AF222718.1	NT	Chrysodidymus synuroides mitochondrion, complete genome
3147	13072	22873	1.03	2.9E-01	AF078111.1	NT	Xenopus laevis transcription factor E2F mRNA, complete cds
3213	13137	22939	2.29	2.9E-01	AW754239.1	EST_HUMAN	PM1-CT0326-171299-001-f12 CT0326 Homo sapiens cDNA
3213	13137	22940	2.29	2.9E-01	AW754239.1	EST_HUMAN	PM1-CT0326-171299-001-f12 CT0326 Homo sapiens cDNA

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3821	13733	23522	1.28	2.9E-01	AI610836.1	EST_HUMAN	tp21a1.1.x1 NCL_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2188412 3' similar to gb:D15050 NIL-2-A
3994	13901		0.82	2.9E-01	AW002802.1	EST_HUMAN	ZINC FINGER PROTEIN (HUMAN); contains element L1 repetitive element;
4384	14280	24059	1.01	2.9E-01	AA284468.1	EST_HUMAN	wr02f10.x1 NCL_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2480395 3'
4388	14284	24064	0.78	2.9E-01	AF134119.1	NT	zs57d12.r1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:701591 5' similar to contains Alu repetitive element;
4388	14284	24065	0.78	2.9E-01	AF134119.1	NT	Mus musculus SKD1 (Skd1) gene, complete cds
4729	14615	24401	0.92	2.9E-01	AB019029.1	NT	Mus musculus SKD1 (Skd1) gene, complete cds
5218	15141		1.49	2.9E-01	R37485.1	EST_HUMAN	Mus musculus gene, complete cds, similar to EXLM1
5522	15440	25504	4.45	2.9E-01	X56098.1	NT	y77e12.s1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:28291 3'
5522	15440	25505	4.45	2.9E-01	X56098.1	NT	B. subtilis levanase operon levD, levE, levF, levG and sacC (partial) genes for fructose phosphotransferase system polypeptides P16, 18, 28, 30 and levanase
5529	15446	25513	5.83	2.9E-01	6679682	NT	B. subtilis levanase operon levD, levE, levF, levG and sacC (partial) genes for fructose phosphotransferase system polypeptides P16, 18, 28, 30 and levanase
5818	15724	25838	2.24	2.9E-01	U03420.1	NT	Mus musculus Eph receptor A8 (Epha8), mRNA
6171	15128	24847	1.51	2.9E-01	AF142329.1	NT	Bos taurus myosin I mRNA, complete cds
6218	16084	26234	2.52	2.9E-01	Q04399	SWISSPROT	Mus musculus Filin protein (Filin) gene, complete cds; and Lgih protein (Lgih) gene, partial cds PUTATIVE MULTICOPPER OXIDASE YDR506C
6249	16115	26267	1.74	2.9E-01	AF100956.1	NT	Mus musculus major histocompatibility locus class II region; Fas-binding protein Daxx (DAXX) gene, partial cds; Bing1 (BING1), tapasin (tapasin), RalGDS-like factor (RLF), KE2 (KE2), BING4 (BING4), beta1, 3- galactosyl transferase (beta1,3-galactosyl tr>
6619	16499	26686	1.76	2.9E-01	BE540422.1	EST_HUMAN	601068830F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3452287 5'
6619	16499	26687	1.76	2.9E-01	BE540422.1	EST_HUMAN	601068830F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3452287 5'
8267	18147	28387	1.96	2.9E-01	AF128843.1	NT	Trypanosoma cruzi stage-specific surface glycoprotein gp82 (gp82) mRNA, partial cds
8502	18375	28639	2.69	2.9E-01	V01394.1	NT	Torpedo californica mRNA encoding acetylcholine receptor gamma subunit
8502	18375	28640	2.69	2.9E-01	V01394.1	NT	Torpedo californica mRNA encoding acetylcholine receptor gamma subunit
8864	18676	28965	1.77	2.9E-01	AA935373.1	EST_HUMAN	my35h02.s1 NCL_CGAP_P12 Homo sapiens cDNA clone IMAGE:1273779 similar to contains LTR8.12 LTR8 repetitive element;
8866	18678	28967	4.54	2.9E-01	AL139078.2	NT	Campylobacter jejuni NCTC11168 complete genome; segment 5/6
9514	19127	25260	1.53	2.9E-01	AW005671.1	EST_HUMAN	wz88f05.x1 NCL_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2565921 3' similar to contains element MER29 repetitive element;
9602	19184	25248	2.74	2.9E-01	AF092453.1	NT	Homo sapiens TNF-a-inducible RNA binding protein (TIRP) gene, complete cds
9644	19212		1.33	2.9E-01	BE788199.1	EST_HUMAN	601482059F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3884559 5'
9883	19367	25188	4.86	2.9E-01	Y08937.1	NT	Chlamydomonas reinhardtii mRNA for nitrite reductase structural locus
9883	19367	25189	4.86	2.9E-01	Y08937.1	NT	Chlamydomonas reinhardtii mRNA for nitrite reductase structural locus

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556	10497		1.84	2.8E-01	U67136.1	NT	Rattus norvegicus A-kinase anchoring protein AKAP150 mRNA, complete cds
1067	10983	20828	2.47	2.8E-01	AF168050.1	NT	Gultra guira oocyte maturation factor Mos (c-mos) gene, partial cds
1256	11163	21013	1.1	2.8E-01	BE313442.1	EST_HUMAN	601148733F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3163688 5'
1256	11163	21014	1.1	2.8E-01	BE313442.1	EST_HUMAN	601148733F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3163688 5'
1269	11176	21025	1.01	2.8E-01	D86550.1	NT	Human mRNA for serine/threonine protein kinase, complete cds
1696	11598	21470	1.55	2.8E-01	AW860020.1	EST_HUMAN	QV1-C10364-120200-065-b05 CT0364 Homo sapiens cDNA
1966	11860	21750	1.77	2.8E-01	AL047620.1	EST_HUMAN	DKFZp586l2321_r1 586 (synonym: hufe1) Homo sapiens cDNA clone DKFZp586l2321
2084	11974	21869	1.47	2.8E-01	AW511195.1	EST_HUMAN	hd44803.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2912333 3'
2423	12300	22197	2.94	2.8E-01	AE000494.1	NT	Escherichia coli K-12 MG1655 section 384 of 400 of the complete genome
2423	12300	22198	2.94	2.8E-01	AE000494.1	NT	Escherichia coli K-12 MG1655 section 384 of 400 of the complete genome
2500	12375		2.47	2.8E-01	AL161565.2	NT	Arabidopsis thaliana DNA chromosome 4, config fragment No. 65
2630	12498	22388	1.37	2.8E-01	AB020975.1	NT	Arabidopsis thaliana mRNA for lipoytransferase, complete cds
2940	12867		1.49	2.8E-01	AF179480.1	NT	Toxoplasma gondii 90kDa heat-shock protein (HSP90) mRNA, partial cds
2941	12868	22667	2.48	2.8E-01	Z14037.1	NT	B.taurus microsatellite (ETH121)
2941	12868	22668	2.48	2.8E-01	Z14037.1	NT	B.taurus microsatellite (ETH121)
3332	13252	23057	1.1	2.8E-01	AP000004.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 777001-994000 nt. position (47)
3915	13824	23604	1.75	2.8E-01	AE001180.1	NT	Borrelia burgdorferi (section 66 of 70) of the complete genome
4103	14003		2.21	2.8E-01	AI090868.1	EST_HUMAN	ov44g10.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1640226 3' similar to contains Alu repetitive element/contains element MER22 repetitive element;
4352	14248	24034		2.8E-01	AL021127.2	NT	Mus musculus chromosome X configa; putative Magea9 gene, Caltractin, NAD(P) steroid dehydrogenase and Zinc finger protein 185
4357	14253	24038	2.2	2.8E-01	P13615	SWISSPROT	RNA POLYMERASE BETA SUBUNIT (LARGE STRUCTURAL PROTEIN) (L PROTEIN)
4673	14559	24352	1.03	2.8E-01	D15050.1	NT	Human mRNA for transcription factor AREB6, complete cds
4673	14559	24353	1.03	2.8E-01	D15050.1	NT	Human mRNA for transcription factor AREB6, complete cds
4722	14608	24394	2.8	2.8E-01	AF030154.1	NT	Bovine adenovirus 3 complete genome
4755	14640	24427	1.54	2.8E-01	BF528188.1	EST_HUMAN	602042601F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4180129 5'
4787	14672	24459	1.7	2.8E-01	AI272699.1	EST_HUMAN	q159c11.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1876628 3' similar to contains Alu repetitive element/contains element LTR5 repetitive element;
5252	19440	24948	21.36	2.8E-01	AA349997.1	EST_HUMAN	EST157072 Infant brain Homo sapiens cDNA 5' end
5443	15363	25419	2.33	2.8E-01	AB016925.1	NT	Homo sapiens OCTN2 gene, complete cds
5770	15677	25784	1.44	2.8E-01	AF003124.1	NT	Mesembryanthemum crystallinum fructose-bisphosphate aldolase mRNA, complete cds
5770	15677	25785	1.44	2.8E-01	AF003124.1	NT	Mesembryanthemum crystallinum fructose-bisphosphate aldolase mRNA, complete cds
6038	15941	26073	7.67	2.8E-01	BF511215.1	EST_HUMAN	U1H-B14-aci-f-04-0-U1.st NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3085182 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6713	16593	26781	1.24	2.8E-01	AI346126.1	EST_HUMAN	qp48h01.x1 NCI_CGAP_Co8 Homo sapiens cDNA clone IMAGE:1926289 3' similar to gb:X06323_cds1 MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L3 (HUMAN);
6713	16593	26782	1.24	2.8E-01	AI346126.1	EST_HUMAN	qp48h01.x1 NCI_CGAP_Co8 Homo sapiens cDNA clone IMAGE:1926289 3' similar to gb:X06323_cds1 MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L3 (HUMAN);
6778	16657	26847	2.39	2.8E-01	U51688.1	NT	Homo sapiens lanosterol 14-alpha demethylase cytochrome P450 (CYP51) gene, exon 5
6994	16871		7.25	2.8E-01	BF347847.1	EST_HUMAN	602022987F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4158525 5'
7311	17187	27388	1.35	2.8E-01	AF080592.1	NT	Mus musculus centrin (Cetn2) gene, complete cds
7600	17451		1.15	2.8E-01	L13654.1	NT	Lycopodium esculentum peroxidase (TPX1) mRNA, complete cds
7789	17639	27872	2.79	2.8E-01	7706163	NT	Homo sapiens hypothetical protein (LOC51319), mRNA
8126	18014	28261	2.27	2.8E-01	BF241082.1	EST_HUMAN	601880794F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4109350 5'
8126	18014	28262	2.27	2.8E-01	BF241082.1	EST_HUMAN	601880794F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4109350 5'
8153	18041	28291	3.01	2.8E-01	BF695970.1	EST_HUMAN	601852148F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4076026 5'
8254	18134	28382	2.62	2.8E-01	AF051682.1	NT	Drosophila heteronema fruitless (fru) gene, alternative splice products, 5' flanking region, exons 1 through 7 and complete cds
8599	18466		3.49	2.8E-01	BF674023.1	EST_HUMAN	602137418F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4273853 5'
9552	19150		6.37	2.8E-01	D83329.1	NT	Mus musculus DNA for prostaglandin D2 synthase, complete cds
9657	19219	25236	3.11	2.8E-01	BE178699.1	EST_HUMAN	PM4-HT0606-030400-001-a07 HT0606 Homo sapiens cDNA
9826	19651		1.69	2.8E-01	11433629	NT	Homo sapiens CDC42-binding protein kinase beta (DMPK-like) (CDC42BPB), mRNA
468	10411	20230	2.33	2.7E-01	Y17324.1	NT	Rattus norvegicus CDK104 mRNA
597	10533	20341	3.14	2.7E-01	AA450061.1	EST_HUMAN	z39b10.s1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:788827 3' similar to contains Alu repetitive element;
1240	11147	20996	1.49	2.7E-01	AB004906.1	NT	Ipomoea purpurea transposable element Tip100 gene for transposase, complete cds
1604	11509		1.73	2.7E-01	X79815.1	NT	G.lambia SR2 gene
1698	11600	21471	2.96	2.7E-01	W58067.1	EST_HUMAN	z422h10.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:341443 5'
1738	11639	21507	1.25	2.7E-01	P03341	SWISSPROT	GAG POLYPROTEIN [CONTAINS: INNER COAT PROTEIN P12; CORE PROTEIN P15; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10]
2088	12712		2.38	2.7E-01	AF047575.1	NT	Rattus norvegicus vesicular monamine transporter type 2, promoter region and exon 1
2316	12197	22094	8.78	2.7E-01	Y13868.1	NT	Feline immunodeficiency virus env gene, isolate ITTO088PU (M88), partial repetitive element;
2406	12283	22180	3.51	2.7E-01	AI310858.1	EST_HUMAN	ta43c11.x2 NCI_CGAP_Lu25 Homo sapiens cDNA clone IMAGE:2046836 3' similar to contains element L1
2956	12883		1.25	2.7E-01	BF088284.1	EST_HUMAN	CM1-HT0875-060300-385-e05 HT0875 Homo sapiens cDNA
3929	13838	23618	1.88	2.7E-01	AI928015.1	EST_HUMAN	w092e11.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2462828 3'
3943	13951	23626	2.31	2.7E-01	L77569.1	NT	Homo sapiens D(George syndrome critical region, telomeric end
4796	14681	24468	0.89	2.7E-01	L27516.1	NT	Triticum aestivum (Wcs66) gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4973	14848		3.5	2.7E-01	AW856131.1	EST_HUMAN	RC1-CT0286-230200-016-e03 CT0286 Homo sapiens cDNA
5221	15144	24838	3.49	2.7E-01	P17277	SWISSPROT	HOMEOBOX PROTEIN HOX-A4 (CHOX-1.4)
6064	16047	26192	2.25	2.7E-01	Q61554	SWISSPROT	FIBRILLIN 1 PRECURSOR
6527	16386	26565	2.23	2.7E-01	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
6527	16386	26566	2.23	2.7E-01	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
7378	17247	27453	10.08	2.7E-01	O83809	SWISSPROT	THREONYL-TRNA SYNTHETASE (THREONINE-TRNA LIGASE) (THRRS)
7378	17247	27454	10.08	2.7E-01	O83809	SWISSPROT	THREONYL-TRNA SYNTHETASE (THREONINE-TRNA LIGASE) (THRRS)
7379	17248		2.24	2.7E-01	P37928	SWISSPROT	FIMBRIN W PROTEIN
7801	17651	27888	1.29	2.7E-01	AF091848.1	NT	Oryctolagus cuniculus calgranulin C mRNA, partial cds
7827	17677	27921	1.93	2.7E-01	AF087434.1	NT	Mus musculus transcription factor NF-ATc isoform a (NF-ATc) mRNA, complete cds
8187	18073	28322	1.76	2.7E-01	AV705043.1	EST_HUMAN	AV705043 ADB Homo sapiens cDNA clone ADBCOD05 5'
8187	18073	28323	1.76	2.7E-01	AV705043.1	EST_HUMAN	AV705043 ADB Homo sapiens cDNA clone ADBCOD05 5'
8197	18082	28333	4.09	2.7E-01	AJ133269.1	NT	Homo sapiens caveolin-1/2 locus, Contig1, D7S522, genes CAV2 (exons 1, 2a, and 2b), CAV1 (exons 1 and 2)
9366	19034		1.27	2.7E-01	X95267.1	NT	G. gallus mRNA for ryanodine receptor type 3
9810	19320		2.15	2.7E-01	AF217491.1	NT	Homo sapiens fragile 16D oxidoreductase (FOR) gene, exon 6
462	12867	20224	1.54	2.6E-01	P78411	SWISSPROT	IROQUOIS-CLASS HOMEODOMAIN PROTEIN IRX-2
472	10416		1.39	2.6E-01	D16459.1	NT	Bos taurus mRNA for mb-1, complete cds
1371	11277	21133	2.23	2.6E-01	BE885087.1	EST_HUMAN	601510838F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912345 5'
1418	11324	21188	0.97	2.6E-01	AB013290.1	NT	Glycine max pseudogene for Bd 30K
1854	11750	21624	8.59	2.6E-01	AL161472.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 2
1854	11750	21625	8.59	2.6E-01	AL161472.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 2
							bb04d10.x1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:2958451 3' similar to gb:M36072 60S
							RIBOSOMAL PROTEIN L7A (HUMAN); gb:M14689_cds1 Mouse surfeit locus surfeit 3 protein gene (MOUSE);
2046	11937		9.9	2.6E-01	AW733152.1	EST_HUMAN	Human prealbumin gene, complete cds
2106	11995	21895	1.2	2.6E-01	M11844.1	NT	B. maritimus tbcL gene
2424	12301		2.68	2.6E-01	Y12996.1	NT	601126016F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:2690043 5'
2499	12374		9.68	2.6E-01	BE272440.1	EST_HUMAN	EST386635 IMAGE:2690043 5'
3053	12980		1.03	2.6E-01	AW974531.1	EST_HUMAN	EST386635 IMAGE:2690043 5'
							h30c02.x1 NC1_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3174914 3' similar to contains L1.13 L1 repetitive element;
3485	13401		0.94	2.6E-01	BE217816.1	EST_HUMAN	Bacteriophage T2 DNA-(adenine-N6)methyltransferase (dam) gene, complete cds
3532	13448	23245	1.12	2.6E-01	M22342.1	NT	

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3591	13505	23295	1.7	2.6E-01	AF229118.1	NT	Homo sapiens acetylcholinesterase collagen-like tail subunit (COLQ) gene, exons 1A, 2, 3, 4, and 5
3651	13565	23351	0.9	2.6E-01	AB017446.1	NT	Rattus norvegicus mRNA for organic anion transporter 3, complete cds
4010	13916	23691	1	2.6E-01	AW959510.1	EST_HUMAN	EST371580 IMAGE resequencing, MAGF Homo sapiens cDNA
4062	13964	23742	13.13	2.6E-01	BE080598.1	EST_HUMAN	QV1-BT0630-040400-132-e03 BT0630 Homo sapiens cDNA
4259	14158	23935	0.95	2.6E-01	AF175293.1	NT	Enterococcus faecium strain N97-330 vanD glycopeptide resistance gene cluster, complete cds; and unknown gene
4393	14289	24072	0.84	2.6E-01	AB021180.1	NT	Gallus gallus mRNA for skeletal myosin heavy chain, complete cds
4393	14289	24073	0.84	2.6E-01	AB021180.1	NT	Gallus gallus mRNA for skeletal myosin heavy chain, complete cds
4448	14342	24134	1.17	2.6E-01	AA457617.1	EST_HUMAN	aa89d07.r1 Stragene fetal retina 937202 Homo sapiens cDNA clone IMAGE:838477 5'
4548	14441	24224	1.63	2.6E-01	U01103.1	NT	Arabidopsis thaliana PSI type III chlorophyll <i>alb</i> -binding protein (Lhca3*) mRNA, complete cds
4616	14504	24292	1.28	2.6E-01	AF142703.1	NT	Ophrestia radicea maturase-like protein (matK) gene, complete cds; chloroplast gene for chloroplast product
4898	14776	24554	3.56	2.6E-01	H04858.1	EST_HUMAN	y51e05.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:152288 5'
5051	14923	24696	0.86	2.6E-01	P08503	SWISSPROT	ACYL-COA DEHYDROGENASE, MEDIUM-CHAIN SPECIFIC, MITOCHONDRIAL PRECURSOR (MCAD)
5700	19764		2.03	2.6E-01	AE001811.1	NT	Thermotoga maritima section 123 of 136 of the complete genome
5763	15670	25777	1.93	2.6E-01	AI582557.1	EST_HUMAN	ts02e12.x1 NCI_CGAP_Par1 Homo sapiens cDNA clone IMAGE:2227438 3' similar to SW:NDF1_RAT Q64289 NEUROGENIC DIFFERENTIATION FACTOR 1 ;contains element LTR1 repetitive element ;
5763	15670	25778	1.93	2.6E-01	AI582557.1	EST_HUMAN	ts02e12.x1 NCI_CGAP_Par1 Homo sapiens cDNA clone IMAGE:2227438 3' similar to SW:NDF1_RAT Q64289 NEUROGENIC DIFFERENTIATION FACTOR 1 ;contains element LTR1 repetitive element ;
6552	16410	26588	1.52	2.6E-01	R10365.1	EST_HUMAN	y37a03.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:129004 3' similar to gb:X12517 U1 SMALL NUCLEAR RIBONUCLEOPROTEIN C (HUMAN);
6585	16465	26656	1.27	2.6E-01	R02411.1	EST_HUMAN	ye82a07.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:124212 5'
6852	16731	26925	3.01	2.6E-01	BF343588.1	EST_HUMAN	602014422F1 NCI_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4150396 5'
6900	16779	26973	2.04	2.6E-01	Q10199	SWISSPROT	HYPOTHETICAL 75.2 KD PROTEIN C11C11.02 IN CHROMOSOME II
7046	16923	27112	4.34	2.6E-01	BE830339.1	EST_HUMAN	RC5-ET0082-310500-021-F10 ET0082 Homo sapiens cDNA
7046	16923	27113	4.34	2.6E-01	BE830339.1	EST_HUMAN	RC5-ET0082-310500-021-F10 ET0082 Homo sapiens cDNA
7854	17704		1.16	2.6E-01	Q28295	SWISSPROT	VON WILLEBRAND FACTOR PRECURSOR (VWF)
8812	18625		93.65	2.6E-01	X51755.1	NT	Human lambda-immunoglobulin constant region complex (germline)
9136	18892		1.98	2.6E-01	10190655	NT	Mus musculus jerky (Jrk), mRNA
9328	19655		1.92	2.6E-01	BE883491.1	EST_HUMAN	601511052F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912612 5'
9395	19053	25309	2.6	2.6E-01	AF316896.1	NT	Homo sapiens Na/K-ATPase gamma subunit (FX/D2) gene, complete cds, alternatively spliced

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9833	19333		6.03	2.6E-01	AF141325.2	NT	Homo sapiens inositol polyphosphate 1-phosphatase (INPP1) gene, complete cds
9999	19376		1.5	2.6E-01	Q01631	SWISSPROT	ADENYLATE CYCLASE (ATP PYROPHOSPHATE-LYASE) (ADENYLYL CYCLASE)
241	10209	20025	2.12	2.5E-01	4502296	NT	Homo sapiens ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit (ATP5D), nuclear gene encoding mitochondrial protein, mRNA
242	10209	20025	1.86	2.5E-01	4502296	NT	Homo sapiens ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit (ATP5D), nuclear gene encoding mitochondrial protein, mRNA
255	10221		3.24	2.5E-01	M26501.1	NT	Starfish (P. ochraceus) cytoplasmic actin gene, complete cds
815	10743	20589	1.32	2.5E-01	U09864.1	NT	Mus musculus ICR/Swiss glycerinaldehyde 3-phosphate dehydrogenase (Gapd-S) gene, complete cds
1044	10962		1.86	2.5E-01	AE002156.1	NT	Ureaplasma urealyticum section 57 of 59 of the complete genome
1105	11021	20864	9.5	2.5E-01	T89837.1	EST_HUMAN	ye11g07.r1 Striatogene lung (#937210) Homo sapiens cDNA clone IMAGE:117468 5'
1503	11407	21266	0.85	2.5E-01	AL115624.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
1697	11599		5.43	2.5E-01	4885406	NT	Homo sapiens hyperpolarization activated cyclic nucleotide-gated potassium channel 4 (HCN4) mRNA
1840	12706	21612	0.88	2.5E-01	BE696604.1	EST_HUMAN	PM4-CT0400-310700-005-d08 CT0400 Homo sapiens cDNA
1840	12706	21613	0.88	2.5E-01	BE696604.1	EST_HUMAN	PM4-CT0400-310700-005-d08 CT0400 Homo sapiens cDNA
2357	12237		8.29	2.5E-01	AE000675.1	NT	Aquifex aeolicus section 7 of 109 of the complete genome
2446	12323		1.35	2.5E-01	AA251987.1	EST_HUMAN	zs11a12.r1 NCJ CGAP_GCB1 Homo sapiens cDNA clone IMAGE:684862 5'
2597	12466	22359	0.97	2.5E-01	X95310.1	NT	B. taurus mRNA for D-aspartate oxidase
3366	13285		2.87	2.5E-01	AW973471.1	EST_HUMAN	EST385464 IMAGE resequences, MAGM Homo sapiens cDNA
3490	13406	23211	0.86	2.5E-01	AF233875.1	NT	Danio rerio peptide YY precursor gene, complete cds
3502	13419	23220	7.93	2.5E-01	AL161517.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 29
3774	13686	23468	1.15	2.5E-01	AI741483.1	EST_HUMAN	wg11c07.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2364780 3'
3774	13686	23469	1.15	2.5E-01	AI741483.1	EST_HUMAN	wg11c07.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2364780 3'
3977	13884		0.83	2.5E-01	P32323	SWISSPROT	A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR
4222	14120		1.2	2.5E-01	Q03314	SWISSPROT	RHIB PROTEIN
4514	14407	24193	0.96	2.5E-01	AF242431.1	NT	Mus musculus neuronal apoptosis inhibitory protein 6 (Naip6) gene, complete cds; and Naip3 gene, exons 2-9 and 11-16
4643	14531		1.14	2.5E-01	Q27225	SWISSPROT	MOLT-INHIBITING HORMONE PRECURSOR (MIH)
4649	14535	24324	3.78	2.5E-01	AF007788.1	NT	Choristoneura fumiferana diapause associated protein 2 (DAP2) mRNA, complete cds
4672	14558	24351	2.19	2.5E-01	AE004416.1	NT	Vibrio cholerae chromosome II, section 73 of 93 of the complete chromosome
4698	14584		3.16	2.5E-01	AJ230113.1	NT	Mus musculus annexin V gene, intron 4 segment containing 5' LTR and gag portion of MuERV-L (murine endogenous retrovirus) element
4726	14612	24398	0.79	2.5E-01	BE896785.1	EST_HUMAN	601437468F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3922600 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4750	14635	24421	0.89	2.5E-01	AB011070.1	NT	Mus musculus gene for uncoupling protein 3, 5'-flanking region and partial 5'UTR
5169	15035	24802	0.86	2.5E-01	AW663183.1	EST_HUMAN	hh75f09.y1 NCL_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2968649 5' similar to contains TAR1.12 TAR1 repetitive element;
5169	15035	24803	0.86	2.5E-01	AW663183.1	EST_HUMAN	hh75f09.y1 NCL_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2968649 5' similar to contains TAR1.12 TAR1 repetitive element;
5264	15186	24962	11.62	2.5E-01	S83390.1	NT	T3 receptor-associating cofactor-1 [human, fetal liver, mRNA, 2930 nt]
6366	16229		1.32	2.6E-01	AF134119.1	NT	Mus musculus SKD1 (Skd1) gene, complete cds
6500	16359	26532	3.73	2.9E-01	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
6583	16463	26555	2.99	2.5E-01	BF109040.1	EST_HUMAN	7157a03.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3525389 3'
6788	16667	26858	2.25	2.5E-01	BF038595.1	EST_HUMAN	601459238F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862809 5'
7020	16897	27087	3.95	2.5E-01	H53236.1	EST_HUMAN	yq84f07.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:202501 5'
7481	17351	27554	16.11	2.6E-01	U89651.2	NT	Homo sapiens matrix metalloproteinase MMP Rasi-1 gene, promoter region
7481	17351	27555	16.11	2.5E-01	U89651.2	NT	Homo sapiens matrix metalloproteinase MMP Rasi-1 gene, promoter region
7522	17341	27547	2.04	2.5E-01	AF085164.1	NT	Hordeum vulgare receptor-like kinase LRK10 gene, partial cds
7522	17341	27548	2.04	2.5E-01	AF085164.1	NT	Hordeum vulgare receptor-like kinase LRK10 gene, partial cds
7814	17664	27904	1.5	2.5E-01	AW581997.1	EST_HUMAN	RC3-ST0186-130100-015-a07 ST0186 Homo sapiens cDNA
8010	17860	28105	1.62	2.5E-01	AW152246.1	EST_HUMAN	xg40c10.x1 NCL_CGAP_U1 Homo sapiens cDNA clone IMAGE:2630034 3' similar to contains Alu repetitive element; contains element MSR1 repetitive element;
8011	17861	28106	1.68	2.5E-01	X58491.1	NT	Mouse L1Md LINE DNA
8426	18300	28556	2.32	2.5E-01	D50914.1	NT	Human mRNA for KIAA0124 gene, partial cds
9074	18851	29117	2.45	2.5E-01	AF200528.1	NT	Zea mays cellulose synthase-4 (Cesa-4) mRNA, complete cds
9100	19729		4.2	2.5E-01	AL161541.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 41
9559	19581	25072	1.28	2.5E-01	AF170072.1	NT	Spodoptera frugiperda CALNUC mRNA, complete cds
541	10482	20292	1.53	2.4E-01	AA936316.1	EST_HUMAN	on70404.s1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1562023 3'
830	10757	20608	2.38	2.4E-01	BF676124.1	EST_HUMAN	602132442F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4271578 5'
1282	11190	21041	17.41	2.4E-01	AJ289880.1	NT	Homo sapiens KIAA0851 gene (partial), XT3 gene and LZTFL1 gene
1282	11190	21042	17.41	2.4E-01	AJ289880.1	NT	Homo sapiens KIAA0851 gene (partial), XT3 gene and LZTFL1 gene
1362	11268	21123	1.04	2.4E-01	Y17293.1	NT	Homo sapiens FLI-1 gene, partial
1808	11705		24.08	2.4E-01	AF267753.1	NT	Mesembryanthemum crystallinum putative potassium channel protein Mkt1p mRNA, complete cds
1858	11754	21629	1.41	2.4E-01	AF251708.1	NT	Zaocys dhumnades fructose-1,6-bisphosphatase mRNA, complete cds
2091	11980	21875	0.88	2.4E-01	AF111168.2	NT	Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds; and unknown genes
2122	12010		1.16	2.4E-01	P45384	SWISSPROT	IMMUNOGLOBULIN A1 PROTEASE PRECURSOR (IGA1 PROTEASE)
2215	12101	22005	2.01	2.4E-01	AE000680.1	NT	Aquifex aeolicus section 12 of 109 of the complete genome

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2332	12213	22111	0.85	2.4E-01	BF002171.1	EST_HUMAN	7h23d04.x1 NCL_CGAP_Co16 Homo sapiens cDNA clone IMAGE:3316807 3' similar to SW:PRSB_XENLA
2491	12366	22280	1.63	2.4E-01	Z36534.1	NT	O42586 26S PROTEASE REGULATORY SUBUNIT 6A ;
2734	12596	22491	2.14	2.4E-01	X71783.1	NT	D.discoideum (Ax3-K) ponA gene
2756	12618	22510	6.68	2.4E-01	AF030154.1	NT	S.pombe swi6 gene
3093	13020		2.82	2.4E-01	U72726.1	NT	Bovine adenovirus 3 complete genome
3109	13035	22831	1.85	2.4E-01	X74209.1	NT	Oryza longistaminata receptor kinase-like protein, family member D, and retrofit (gag/pol) genes, complete cds
4817	14700	24486	0.88	2.4E-01	BE160080.1	EST_HUMAN	H.sapiens AGT gene, PstI fragment of intron 4
4981	14856	24622	50.15	2.4E-01	D00944.1	NT	QV1-HT0412-020400-136-b10 HT0412 Homo sapiens cDNA
5469	15389	25451	7.53	2.4E-01	AF091216.1	NT	Hepatitis C virus genomic RNA for polyprotein, complete cds
5469	15389	25452	7.53	2.4E-01	AF091216.1	NT	Mus musculus Wrm protein (Wrm) gene, complete cds
							Mus musculus Wrm protein (Wrm) gene, complete cds
5593	15508	25583	2.13	2.4E-01	BF592336.1	EST_HUMAN	7i54d04.x1 NCL_CGAP_Br16 Homo sapiens cDNA clone IMAGE:3338503 3' similar to SW:SFR4_HUMAN
5642	15555	25648	2.66	2.4E-01	AF035546.1	NT	Q08170 SPLICING FACTOR, ARGININE/SERINE-RICH 4 ; contains element TAR1 TAR1 repetitive element
5705	15613	25714	2.15	2.4E-01	7661801	NT	Drosophila melanogaster p38a MAP kinase gene, complete cds
5937	15842	25966	1.79	2.4E-01	AI698989.1	EST_HUMAN	Homo sapiens HSPC142 protein (HSPC142), mRNA
6345	16208	26371	8.87	2.4E-01	L43001.1	NT	wc62c11.x1 NCL_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2323220 3' similar to gb:J03464
6860	16739	26931	1.62	2.4E-01	AJ012585.1	NT	PROCOLLAGEN ALPHA 2(I) CHAIN PRECURSOR (HUMAN);
							Bos taurus guanylyl cyclase-activating protein 2 (guca2) mRNA, complete cds
							Tetrahymena thermophila macronuclear gene encoding ribosomal protein L3, exons 1-2
7517	17305	27511	5.72	2.4E-01	AI693515.1	EST_HUMAN	wd43e02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2330906 3' similar to contains
7965	17815	28056	1.93	2.4E-01	Q03692	SW/ISSPROT	MER22.b1 TAR1 repetitive element ;
8149	18037	28285	3.63	2.4E-01	AL181494.2	NT	COLLAGEN ALPHA 1(X) CHAIN PRECURSOR
8209	18093	28347	1.99	2.4E-01	AF030199.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 6
8534	18406		2.42	2.4E-01	Z21647.1	NT	Mus musculus type 1 sigma receptor gene, complete cds
9030	18821	29109	1.55	2.4E-01	AF217491.1	NT	P.asiatica mosaic virus genomic RNA
9162	19526		2.39	2.4E-01	AF004213.1	NT	Homo sapiens fragile 16D oxidoreductase (FOR) gene, exon 6
9222	18945		2.54	2.4E-01	AJ278191.1	NT	Arabidopsis thaliana ethylene-insensitive3-like1 (EIL1) mRNA, complete cds
9439	19509		1.59	2.4E-01	V01507.1	NT	Mus musculus mRNA for putative mc7 protein (mc7 gene)
9650	19716		1.26	2.4E-01	BF229975.1	EST_HUMAN	Gallus gallus gene coding for a-actin
9865	19355		3.35	2.4E-01	AL183281.2	NT	RC3-CT0413-100800-023-b06 CT0413 Homo sapiens cDNA
383	10330	20153	0.9	2.3E-01	S75898.1	NT	Homo sapiens chromosome 21 segment HS21C081 aromatase [P.oephila guttata-zebra finches, ovary, mRNA, 3188 nt]

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
621	10558		4.42	2.3E-01	U39713.1	NT	Mycoplasma genitalium section 35 of 51 of the complete genome
651	10587	20403	19.84	2.3E-01	U67596.1	NT	Methanococcus jannaschii section 139 of 150 of the complete genome
918	10842	20687	3.35	2.3E-01	BE311893.1	EST_HUMAN	601142073F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3505818 5'
1494	11398	21258	1.5	2.3E-01	6677980	NT	Mus musculus vacuolar protein sorting 4b (yeast) (Vps4b), mRNA
1546	11451		0.88	2.3E-01	U22837.2	NT	Yersinia pestis HmsH (hmsH), HmsF (hmsF), HmsR (hmsR), and HmsS (hmsS) genes, complete cds
1586	11490	21351	1.38	2.3E-01	AJ245480.1	NT	Brassica napus sig gene for S-locus glycoprotein, cultivar T2
1614	11518	21378	2.75	2.3E-01	Y10887.2	NT	Mus musculus cdh5 gene, exon 1, partial
1999	11892		1.3	2.3E-01	AJ235333.1	NT	Homo sapiens partial intron 3 of the wild type AF-4/FEL gene
2396	12274	22169	1.56	2.3E-01	BE297718.1	EST_HUMAN	601175562F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531015 5'
2615	12483	22372	1.02	2.3E-01	M11319.1	NT	Human erythropoietin gene, complete cds
2794	11271	21127	0.88	2.3E-01	AB015033.1	NT	Marinilabilla agarivorans gyrB gene for DNA gyrase subunit B, partial cds, strain IFO 14957
2834	12861	22661	1.29	2.3E-01	AA601379.1	EST_HUMAN	no16d06.s1 NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100843 3' similar to contains Alu repetitive element; contains element THR repetitive element;
3045	12972		5.73	2.3E-01	R21732.1	EST_HUMAN	yr21b07.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:130357 3'
3324	13244	23051	1.09	2.3E-01	H69836.1	EST_HUMAN	yr97h10.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:213283 5'
3766	13679	23461	1.11	2.3E-01	S82821.1	NT	GSTA5=glutathione S-transferase Yc2 subunit {5' region, intron 1} [rats, Morris hepatoma cell line, Genomic, 2212 nt, segment 1 of 3]
3856	13767		3.72	2.3E-01	7662133	NT	Homo sapiens KIAA0450 gene product (KIAA0450), mRNA
4253	14152	23926	0.85	2.3E-01	R82252.1	EST_HUMAN	y17f01.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:149017 5'
4300	14198		3.35	2.3E-01	L78789.1	NT	Mus musculus renin (Ren-1c) gene, promoter region
4349	14245	24031	1.02	2.3E-01	D90899.1	NT	Synechocystis sp. PCC6803 complete genome, 1/27, 1-133859
4386	14282	24061	2.08	2.3E-01	AF092535.1	NT	Homo sapiens mitogen-activated protein kinase p38delta (PRKM13) mRNA, complete cds
4454	14348	24140	5.1	2.3E-01	5031984	NT	Homo sapiens nuclear transport factor 2 (placental protein 15) (PP16) mRNA
4956	14668	24455	0.82	2.3E-01	J03280.1	NT	Human phenylethanolamine N-methyltransferase gene, complete cds
5002	14877	24641	0.95	2.3E-01	BF316135.1	EST_HUMAN	601896136F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4125368 5'
5101	14969	24745	0.98	2.3E-01	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
5146	15013	24783	26.95	2.3E-01	AE000240.1	NT	Escherichia coli K-12 MG1655 section 130 of 400 of the complete genome
5246	15169	24942	2.6	2.3E-01	AB040945.1	NT	Homo sapiens mRNA for KIAA1512 protein, partial cds
5332	15252	25074	1.71	2.3E-01	BF058381.1	EST_HUMAN	7k30b06.x1 NCI_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3476699 3' similar to SW:GAG_SMSAV P03330 GAG POLYPROTEIN [CONTAINS: CORE PROTEIN P16; INNER COAT PROTEIN P12; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10] ;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5395	15314	25361	4.83	2.3E-01	X96587.1	NT	C.familiaris rom1 gene
5618	15533	25617	1.87	2.3E-01	AI708840.1	EST_HUMAN	as27e12.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2318446 3' similar to gb:X13238 CYTOCHROME C OXIDASE POLYPEPTIDE VIC PRECURSOR (HUMAN);
5618	15533	25618	1.87	2.3E-01	AI708840.1	EST_HUMAN	as27e12.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2318446 3' similar to gb:X13238 CYTOCHROME C OXIDASE POLYPEPTIDE VIC PRECURSOR (HUMAN);
6111	16005	26142	3.93	2.3E-01	AI718148.1	EST_HUMAN	as42f12.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2319887 3' similar to contains Alu repetitive element;
6384	16246	26408	2.62	2.3E-01	AF175399.1	NT	Glycine max resistance protein LM17 precursor RNA, partial cds
6487	16345		3.19	2.3E-01	6754779	NT	Mus musculus myosin XV (Myo15), mRNA
6491	16349	26519	1.59	2.3E-01	BE888071.1	EST_HUMAN	601511573F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912859 5'
6560	16418		2.9	2.3E-01	N80983.1	EST_HUMAN	za12e08.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:292358 5'
6664	16544	26741	2.28	2.3E-01	M68931.1	NT	Oxytricha nova macronuclear telomere-binding protein alpha subunit (tel-alpha alanine version) gene, complete cds
7657	17507	27732	1.37	2.3E-01	X52124.1	NT	Haemophilus influenzae genes for HincII restriction-modification system (HincII methyltransferase (EC 2.1.1.72) and HincII endonuclease (EC 3.1.21.4))
7712	17562	27787	2.54	2.3E-01	BE173060.1	EST_HUMAN	MFR0-HT0559-240400-014-g11 HT0559 Homo sapiens cDNA
7740	17590	27811	2.26	2.3E-01	AJ293261.1	NT	Rhizobium leguminosarum partial genomic DNA for exopolysaccharide biosynthesis genes
7974	17824		4.95	2.3E-01	BF133577.1	EST_HUMAN	601646159R2 NIH_MGC_59 Homo sapiens cDNA clone IMAGE:4102092 3'
8525	18397	28663	2.94	2.3E-01	AJ250189.1	NT	Mus musculus partial mRNA for muscle protein 534 (mg534 gene)
8525	18397	28664	2.84	2.3E-01	AJ250189.1	NT	Mus musculus partial mRNA for muscle protein 534 (mg534 gene)
8658	18547	28830	2.39	2.3E-01	AE002167.2	NT	Chlamydomonas reinhardtii AR39, section 4 of 94 of the complete genome
9144	18898		2.53	2.3E-01	U45426.1	NT	Borrelia burgdorferi 2.9-6 locus, ORF-A-D genes, complete cds and REP+ gene, partial cds
9232	18951		20.46	2.3E-01	T27231.1	EST_HUMAN	HCOEST44 HT29M6 Homo sapiens cDNA clone HCOE44 5'
9258	19477		1.65	2.3E-01	AA089819.1	EST_HUMAN	chm1424.seq.F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA 5'
9266	18970		2.07	2.3E-01	AW863940.1	EST_HUMAN	PM4-SN0012-030400-001-b06 SN0012 Homo sapiens cDNA
9324	19665	24990	2.05	2.3E-01	AW303623.1	EST_HUMAN	xv21d07.x1 Soares, NFL T. GBC. S1 Homo sapiens cDNA clone IMAGE:2813773 3' similar to TR:Q9Z175 Q9Z175 LVSYL OXIDASE-RELATED PROTEIN 2, contains PTR5:b2 TAR1 repetitive element ;
9358	19708	24905	4.88	2.3E-01	BE882464.1	EST_HUMAN	601507202F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3908689 5'
9407	19090		1.93	2.3E-01	BF663319.1	EST_HUMAN	602144459F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4297719 5'
9456	19088		2.09	2.3E-01	AJ006519.1	NT	Rattus norvegicus mRNA for acid gated ion channel
9549	19088		4.54	2.3E-01	AJ006519.1	NT	Rattus norvegicus mRNA for acid gated ion channel
9793	19310		2.67	2.3E-01	BF475611.1	EST_HUMAN	nac39h12.x1 Lupski, sciatic_nerve Homo sapiens cDNA clone IMAGE:3395950 3' similar to contains element MER38 repetitive element ;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
84	10088	19885	0.96	2.2E-01	AI052190.1	EST_HUMAN	oz14a10.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1675290 3' similar to TR:Q13040 Q13040 ATP-BINDING CASSETTE PROTEIN;
1545	11450	21311	3.13	2.2E-01	AF187850.1	NT	Homo sapiens PPAR delta gene, promoter region
1972	11865	-	0.91	2.2E-01	AF171901.1	NT	Trimeresurus malabaricus cyto gene, partial cds; mitochondrial gene for mitochondrial product
2042	11933	21829	2.78	2.2E-01	M34640.1	NT	Fresh-water sponge Emf1 alpha collagen (COLF1) gene
2354	12234	22131	6.24	2.2E-01	BF677538.1	EST_HUMAN	602085608F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249369 5'
2543	12417	22307	2.41	2.2E-01	BE618258.1	EST_HUMAN	601462629F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866190 5'
2543	12417	22308	2.41	2.2E-01	BE618258.1	EST_HUMAN	601462629F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866190 5'
2853	12781	22570	4.04	2.2E-01	BE155625.1	EST_HUMAN	PM2-HT0353-281299-003-a12 HT0353 Homo sapiens cDNA
2853	12781	22571	4.04	2.2E-01	BE155625.1	EST_HUMAN	PM2-HT0353-281299-003-a12 HT0353 Homo sapiens cDNA
2890	12817	-	1.59	2.2E-01	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
3346	13266	-	2.67	2.2E-01	AL161562.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 62
3743	13655	-	1.05	2.2E-01	AF155728.1	NT	Xiphophorus maculatus truncated Rex1 retrotransposon reverse transcriptase (RT) pseudogene
4007	13913	23688	0.81	2.2E-01	AF213391.1	NT	Mus musculus ATP-binding cassette protein (Abcb8) mRNA, partial cds
4118	14018	-	1.19	2.2E-01	AF119102.1	NT	Drosophila melanogaster UNC-119 (unc-119) gene, complete cds
4125	14025	23800	5.07	2.2E-01	AF155142.1	NT	Mus musculus mixed lineage kinase 3 (Mlik3) and two pore domain K+ channel subunit (Konk6) genes, complete cds
4166	14066	23840	1.97	2.2E-01	AF117340.1	NT	Mus musculus MAP kinase kinase kinase 1 (Mekk1) mRNA, complete cds
4166	14066	23841	1.97	2.2E-01	AF117340.1	NT	Mus musculus MAP kinase kinase kinase 1 (Mekk1) mRNA, complete cds
4258	14157	23933	1.16	2.2E-01	U01307.1	NT	Human scRNA (BC200 beta) pseudogene
4258	14157	23934	1.16	2.2E-01	U01307.1	NT	Human scRNA (BC200 beta) pseudogene
4399	14294	24078	1.09	2.2E-01	Z54148.1	NT	B.abortus bp26 gene
4719	14805	-	1.22	2.2E-01	D50604.1	NT	Human beta-cytoplasmic actin (ACTBP9) pseudogene
4724	14810	24396	2.47	2.2E-01	AA211216.1	EST_HUMAN	zq87cd05.r1 Stralagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:648968 5'
4891	14771	24549	1.19	2.2E-01	M86524.1	NT	Human cystrophin gene
4975	14850	-	1.2	2.2E-01	L13299.1	NT	Mus musculus vinculin gene, exon 3
5513	15431	25495	1.71	2.2E-01	5803002	NT	Homo sapiens diaphanous (Drosophila, homolog) 2 (DIAPH2), transcript variant 156, mRNA
5518	15436	-	3.99	2.2E-01	D64000.1	NT	Synechocystis sp. PCC6803 complete genome, 19/27, 2392729-2538999
6189	16074	26223	10.59	2.2E-01	AV756238.1	EST_HUMAN	AV756238 BM Homo sapiens cDNA clone BMFAHC06 5'
6319	16182	26342	2.01	2.2E-01	M24136.1	NT	Human glycophorin B gene, exon 4
6319	16182	26343	2.01	2.2E-01	M24136.1	NT	Human glycophorin B gene, exon 4
6376	16556	-	2.19	2.2E-01	AF155143.1	NT	Mus musculus nm23-M1 gene, promoter region
7157	17034	27227	4.27	2.2E-01	AE001713.1	NT	Thermotoga maritima section 25 of 136 of the complete genome

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7217	17094		2.29	2.2E-01	AW855039.1	EST_HUMAN	PM3-CT0263-241299-009-b07 CT0263 Homo sapiens cDNA
7270	17147	27341	1.66	2.2E-01	8393247	NT	Mus musculus deformed epidermal autoregulatory factor 1 (Drosophila) (Deaf1), mRNA
7304	17180	27382	1.39	2.2E-01	BF376354.1	EST_HUMAN	MR1-TN0045-110900-006-c02 TN0045 Homo sapiens cDNA
7353	17221	27421	1.4	2.2E-01	W02988.1	EST_HUMAN	za0408.r1 Soares melanocyte 2Nblm Homo sapiens cDNA clone IMAGE:291591 5'
7366	17344	27550	13.13	2.2E-01	P48634	SWISSPROT	LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2)
7397	17315	27522	3.98	2.2E-01	M89643.1	NT	Brachydanio rerio ependymin beta and gamma chains (Epd) gene, complete cds
7648	17498	27720	3.57	2.2E-01	AF197941.1	NT	Funaria hygrometrica chloroplast-localized small heat shock protein (CPsHSP21) mRNA, complete cds; nuclear gene for chloroplast product
7719	17569	27794	2.2	2.2E-01	BF206507.1	EST_HUMAN	601869724F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4100189 5'
8723	18540	28824	4.94	2.2E-01	X01918.1	NT	Drosophila 68C glue gene cluster
8766	17906	28149	2.91	2.2E-01	7706216	NT	Homo sapiens H-2K binding factor-2 (LOC51580), mRNA
9077	18854		2.2	2.2E-01	BE870959.1	EST_HUMAN	601446957F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3850670 5'
9183	19720		3.72	2.2E-01	U82671.2	NT	Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12 (MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), caltractin (CALT), NAD(P)H dehydrogenase-like protein (NSDHL), and L1>
9269	18973		2.34	2.2E-01	AF18843.1	NT	Vitis vinifera cultivar Pinot Noir plasma membrane aquaporin (PIP1a) mRNA, complete cds
9379	15093	24887	2.56	2.2E-01	AW361098.1	EST_HUMAN	RC1-CT0249-141199-021-g04 CT0249 Homo sapiens cDNA
9875	19713		3.75	2.2E-01	AV694801.1	EST_HUMAN	AV694801 GKC Homo sapiens cDNA clone GKCAHB02 5'
955	10879	20727	1.74	2.1E-01	AA569289.1	EST_HUMAN	nm31e1.s1 NCI_CGAP_Lip2 Homo sapiens cDNA clone IMAGE:1061804
958	10881	20729	0.9	2.1E-01	AL161504.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 16
1108	11023		2.16	2.1E-01	AE002314.2	NT	Chlamydia muridarum, section 45 of 85 of the complete genome
1180	11091	20936	1.24	2.1E-01	6754299	NT	Mus musculus interferon (alpha and beta) receptor 2 (Ifnar2), mRNA
1180	11091	20937	1.24	2.1E-01	6754299	NT	Mus musculus interferon (alpha and beta) receptor 2 (Ifnar2), mRNA
1871	11767	21642	1.84	2.1E-01	AA906824.1	EST_HUMAN	ok73e02.s1 NCI_CGAP_GC4 Homo sapiens cDNA clone IMAGE:1519610 3' similar to gb:K02765
2111	12000	21899	3.08	2.1E-01	BF695073.1	EST_HUMAN	COMPLEMENT C3 PRECURSOR (HUMAN);
2894	12821	22613	1.65	2.1E-01	6912445	NT	602083129F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4247503 5'
3736	13648		5.05	2.1E-01	9838361	NT	Homo sapiens potassium voltage-gated channel, subfamily H (seg-related), member 4 (KCNH4), mRNA
3967	13874	23651	1.01	2.1E-01	P11675	SWISSPROT	Beta vulgaris mitochondrion, complete genome
3967	13874	23652	1.01	2.1E-01	P11675	SWISSPROT	IMMEDIATE-EARLY PROTEIN IE180
4279	14178		1.28	2.1E-01	AB033041.1	NT	IMMEDIATE-EARLY PROTEIN IE180
4474	14368	24157	1.21	2.1E-01	AB010273.1	NT	Homo sapiens pshsp47 gene, complete cds
4766	14651	24439	1.26	2.1E-01	AJ009794.1	NT	Homo sapiens hox11 proto-oncogene, exons 1 to 3 and hug-1 gene

Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5134	15001	24772	0.99	2.1E-01	M98261.1	NT	Saccharomyces cerevisiae tau138 (TFC3) gene, complete cds
5243	15167	24938	5.99	2.1E-01	BF672895.1	EST_HUMAN	602152001F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4293001 5'
6123	15970	26106	1.86	2.1E-01	U04642.1	NT	Human olfactory receptor (OR17-2) gene, partial cds
6385	16247		1.97	2.1E-01	AE000972.1	NT	Archaeoglobus fulgidus section 135 of 172 of the complete genome
6535	16393	26572	1.74	2.1E-01	AF000949.1	NT	Canis familiaris keratin (KRT9) gene, complete cds
6559	16417	26596	1.35	2.1E-01	AF068887.1	NT	Glycine max malate dehydrogenase (Mdh-2) gene, nuclear gene encoding mitochondrial protein, partial cds
6559	16417	26597	1.35	2.1E-01	AF068887.1	NT	Glycine max malate dehydrogenase (Mdh-2) gene, nuclear gene encoding mitochondrial protein, partial cds
6705	16585		1.21	2.1E-01	7305030	NT	Mus musculus erythrocyte protein band 4.1-like 3 (Epb4.1b), mRNA
6951	16829	27022	4.78	2.1E-01	U68399.1	NT	Haemophilus influenzae hmcD, putative haemocin processing protein (hmcC), putative ABC transporter (hmcB), putative haemocin structural protein (hmcA), and haemocin immunity protein (hmcI) genes, complete cds
7224	17104	27289	5.88	2.1E-01	Z35786.1	NT	S.cerevisiae chromosome II reading frame ORF YBL025w
7479	17349	27553	2.36	2.1E-01	X97378.1	NT	A.thaliana mRNA for ATRanBP1b protein
7547	17398	27611	1.19	2.1E-01	AB036529.1	NT	Homo sapiens p53R2 gene for ribonucleotide reductase, exon 6
7917	17767	28006	2.49	2.1E-01	Z97067.1	NT	Beta vulgaris mRNA for elongation factor 1-beta
7929	17779	28018	1.49	2.1E-01	P52824	SWISSPROT	DIACYLGLYCEROL KINASE, DELTA (DIGLYCERIDE KINASE) (DGK-DELTA) (DAG KINASE DELTA)
8849	18661		2.31	2.1E-01	11036647	NT	Homo sapiens pancreatic polypeptide 2 (PPY2), mRNA
8862	18674	28964	2.15	2.1E-01	BE180422.1	EST_HUMAN	RC3-HT0622-040500-013-b11 HT0622 Homo sapiens cDNA
9522	19132		1.6	2.1E-01	AF217490.1	NT	Homo sapiens fragile 16D oxido reductase (FOR) gene, exons 8, 9, and partial cds
9730	19634		1.4	2.1E-01	L32598.1	NT	Human granulin gene
9905	19382	25174	1.29	2.1E-01	BE672930.1	EST_HUMAN	7a59a02.x1 NCI_CGAP_G06 Homo sapiens cDNA clone IMAGE:3223034 3'
9979	19436		1.29	2.1E-01	5835904	NT	Salvelinus alpinus mitochondrion, complete genome
193	10165	19983	1.72	2.0E-01	AB017437.1	NT	Gallus gallus mRNA for avena, complete cds
523	10465		2.39	2.0E-01	7705601	NT	Homo sapiens CGI-18 protein (LOC51008), mRNA
684	10617	20440	1.19	2.0E-01	M77085.1	NT	O.cuniculus germline IgH heavy chain V-H pseudogene, allotype V-Ha2
793	10722	20563	1.81	2.0E-01	AF027865.1	NT	Mus musculus Major Histocompatibility Locus class II region
995	10915	20759	1.03	2.0E-01	D90905.1	NT	Synechocystis sp. PCC6803 complete genome, 7/27, 781449-920915
1109	11024	20866	2.57	2.0E-01	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
1234	11141	20993	1.42	2.0E-01	AJ132695.5	NT	Homo sapiens rac1 gene
1286	11194	21047	1.29	2.0E-01	AW384937.1	EST_HUMAN	PM1-HT0422-291/299-002-c06 HT0422 Homo sapiens cDNA
1471	11376	21241	13.51	2.0E-01	4503408	NT	Homo sapiens dystrobrevin, alpha (DTNA), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1534	11438	21295	2.51	2.0E-01	AB007974.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0505
1538	11442	21300	1.59	2.0E-01	AF260700.1	NT	Homo sapiens sodium/iodide symporter mRNA, partial cds
1698	11590		1.82	2.0E-01	AF111170.3	NT	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene
1723	11624		1.64	2.0E-01	U67525.1	NT	Methanococcus jannaschii section 67 of 150 of the complete genome
1847	11743	21618	1.33	2.0E-01	BE871330.1	EST_HUMAN	601449441F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3853330 5'
1847	11743	21619	1.33	2.0E-01	BE871330.1	EST_HUMAN	601449441F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3853330 5'
2299	12181		1.67	2.0E-01	X82877.1	NT	H. sapiens Na+-D-glucose cotransport regulator gene
2861	12789		0.95	2.0E-01	AF074990.1	NT	Homo sapiens full length insert cDNA YH85A11
3442	13359	23166	0.8	2.0E-01	P46607	SWISSPROT	HOMEOBOX PROTEIN GLABRA2 (HOMEOBOX-LEUCINE ZIPPER PROTEIN ATHB-10) (HD-ZIP PROTEIN ATHB-10)
3520	13436		0.89	2.0E-01	AW238005.1	EST_HUMAN	xp15b02.x1 NCI_CGAP_HIN9 Homo sapiens cDNA clone IMAGE:2740395 3' similar to contains element
3646	13560	23346	0.81	2.0E-01	P34641	SWISSPROT	MER21 repetitive element ;
3945	13853	23628	0.8	2.0E-01	X83997.1	NT	CEP-11 PROTEIN
4464	14358		8.47	2.0E-01	BE826165.1	EST_HUMAN	C.parasitica eapC gene
4859	14739	24519	1.07	2.0E-01	AF147083.1	NT	QV4-EN0032-190500-223-e03 EN0032 Homo sapiens cDNA
4972	14947	24616	6.07	2.0E-01	8922080	NT	Homo sapiens gamma-glutamyl hydrolase gene, exons 8 and 9 and complete cds
5041	14913	24687	1.1	2.0E-01	Y19216.1	NT	Homo sapiens hypothetical protein ASH1 (ASH1), mRNA
5342	15263	25089	2.55	2.0E-01	X56800.1	NT	Homo sapiens putative psilHbD pseudogene for hair keratin, exons 1 to 9
5510	15428	25497	2.13	2.0E-01	11432540	NT	Rat SOD-2 gene for manganese-containing superoxide dismutase
5694	15603	25705	5.29	2.0E-01	U15300.1	NT	Homo sapiens dual oxidase-like domains 2 (DUOX2), mRNA
5874	15780	25900	4.31	2.0E-01	X61033.1	NT	Saccharomyces cerevisiae Hal5p (HAL5) mRNA, complete cds
5934	15839	25962	3.54	2.0E-01	AW360865.1	EST_HUMAN	M. auratus mu class glutathione transferase gene
6937	16517		6.95	2.0E-01	AF028026.1	NT	PM1-CT0247-141099-001-g08 CT0247 Homo sapiens cDNA
6772	16651	26839	4.18	2.0E-01	X91151.1	NT	Andes virus strain O123193 glycoprotein G1 and G2 precursor, gene, partial cds
7511	17299		4.39	2.0E-01	AE001278.1	NT	M. musculus scp2 gene exon 14
7692	17542		2.07	2.0E-01	AF143692.1	NT	Chlamydia trachomatis section 5 of 87 of the complete genome
7774	17624	27857	1.95	2.0E-01	AF086907.1	NT	Homo sapiens filamin 2 (FLN2) mRNA, complete cds
7774	17624	27858	1.95	2.0E-01	AF086907.1	NT	Arabidopsis thaliana root gravitropism control protein (PIN2) gene, complete cds
8214	18098	28350	2.7	2.0E-01	D89088.1	NT	Arabidopsis thaliana root gravitropism control protein (PIN2) gene, complete cds
8214	18098	28351	2.7	2.0E-01	D89088.1	NT	Salvelinus pluvius mRNA for transferrin, complete cds
9503	19118		1.37	2.0E-01	AF206637.2	NT	Salvelinus pluvius mRNA for transferrin, complete cds
9747	19308	25202	3.22	2.0E-01	AI023592.1	EST_HUMAN	Pimphales promelas liver glucose-6-phosphate-1-dehydrogenase mRNA, partial cds
9769	19288		6.61	2.0E-01	AF078164.2	NT	ov80a10.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1643610 3'
						NT	Homo sapiens Ku70-binding protein (KUB3) mRNA, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9897	19374	25193	1.5	2.0E-01	11528495	NT	Mus musculus fructosamine 3 kinase (Fn3k), mRNA
105	10086		10.35	1.9E-01	7549743	NT	Rattus norvegicus Aryl hydrocarbon receptor nuclear translocator 1 (Ahrnt1), mRNA
349	10308	20126	6	1.9E-01	AF004353.1	NT	Mus musculus pale ear (ep) gene, wild type allele, 3' region, partial cds
640	10577	20392	1.31	1.9E-01	U32581.2	NT	Homo sapiens lambda/iota protein kinase C-interacting protein mRNA, complete cds
640	10577	20393	1.31	1.9E-01	U32581.2	NT	Homo sapiens lambda/iota protein kinase C-interacting protein mRNA, complete cds
647	10584	20400	5.37	1.9E-01	BE070801.1	EST_HUMAN	RC3-BT0502-251199-011-d01 BT0502 Homo sapiens cDNA
648	10584	20400	7.32	1.9E-01	BE070801.1	EST_HUMAN	RC3-BT0502-251199-011-d01 BT0502 Homo sapiens cDNA
970	10893		1.61	1.9E-01	7305180	NT	Mus musculus interleukin 2 receptor, gamma chain (Il2rg), mRNA
1088	11004	20846	9.3	1.9E-01	AA358813.1	EST_HUMAN	EST167784 Fetal lung II Homo sapiens cDNA 5' end
1348	11254	21110	2.3	1.9E-01	AF061282.1	NT	Sorghum bicolor 22 kDa kafirin cluster
1416	11322		3.91	1.9E-01	AF184823.1	NT	Plasmodium vivax reticulocyte binding protein-2 (rbp-2) gene, complete cds
2330	12211	22109	3.31	1.9E-01	8922833	NT	Homo sapiens hypofunctional protein FLJ10581 (FLJ10581), mRNA
2892	12819	22811	3.91	1.9E-01	U66066.1	NT	Sigmodon hispidus p53 gene, partial cds
2908	12834		5.55	1.9E-01	J00922.1	NT	Gallus gallus ovalbumin (Y) gene, complete cds
3349	13269	23072	3.4	1.9E-01	D13197.1	NT	Mouse gene for immunoglobulin diversity region D1
3434	13351	23156	4.63	1.9E-01	R16467.1	EST_HUMAN	yf42f10 r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:129547 5'
3735	13647	23432	0.93	1.9E-01	AF264017.1	NT	Rattus norvegicus arylacetamide deacetylase gene, complete cds
3762	13675	23457	0.96	1.9E-01	P39768	SWISSPROT	PAIR-RULE PROTEIN ODD-PAIRED
3910	13820	23600	3.02	1.9E-01	AB006784.1	NT	Schizosaccharomyces pombe DNA for cytoplasmic dynein heavy chain, complete cds
3992	13899	23676	1.89	1.9E-01	AW754106.1	EST_HUMAN	OM3-CT0315-271199-045-b11 CT0315 Homo sapiens cDNA
4138	14038	23813	1.06	1.9E-01	BE834943.1	EST_HUMAN	MR1-FN0010-290700-007-d04 FN0010 Homo sapiens cDNA
4369	14265	24049	0.89	1.9E-01	AL161493.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 5
4662	14548	24338	0.84	1.9E-01	Z93780.1	NT	Fugu rubripes genes encoding carbamoyl phosphate synthetase III, myosin light chain, MAP2
4912	14791	24566	0.86	1.9E-01	AW849203.1	EST_HUMAN	IL3-CT0215-180200-087-D02 CT0215 Homo sapiens cDNA
4943	14821		1.04	1.9E-01	AF223642.1	NT	Rattus norvegicus chemokine receptor CXCR3 mRNA, complete cds
4962	14837	24605	1.11	1.9E-01	O98239	SWISSPROT	KINESIN-LIKE PROTEIN KIF4
5031	14903	24675	1.03	1.9E-01	AJ251176.1	NT	Phoca vitulina partial aar2B gene for alpha adrenergic receptor 2B
5113	14981	24755	0.99	1.9E-01	Z70296.1	NT	Simonsi elastase HP1 gene
5123	14991		1.19	1.9E-01	A1631199.1	EST_HUMAN	ts93g12.x1 NCI_CGAP_G06 Homo sapiens cDNA clone IMAGE:2238886 3' similar to gb:M21574 ALPHA
5153	15020	24789	0.99	1.9E-01	6679085	NT	PLATELET-DERIVED GROWTH FACTOR RECEPTOR PRECURSOR (HUMAN);
							Mus musculus Notch gene homolog 3, (Drosophila) (Notch3), mRNA
5441	15361		4.28	1.9E-01	AW130149.1	EST_HUMAN	xf29a07.x1 NCI_CGAP_UH1 Homo sapiens cDNA clone IMAGE:2619444 3' similar to gb:M73779 RETINOIC
5466	15386	25446	7.67	1.9E-01	AF127937.1	NT	ACID RECEPTOR ALPHA-1 (HUMAN);
							Homo sapiens DNA polymerase epsilon catalytic subunit protein (POLE1) gene, exon 1a

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5588	15503		2.26	1.9E-01	AU133116.1	EST_HUMAN	AU133116 NT2RP4 Homo sapiens cDNA clone NT2RP4001328 5'
6162	15119		1.7	1.9E-01	R43212.1	EST_HUMAN	y90a12.s1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:31663 3' similar to contains MER13 repetitive element ;
6423	16284	24863	1.43	1.9E-01	U80922.1	NT	Arabidopsis thaliana serine/threonine protein phosphatase type one (TOPP8) gene, complete cds
6449	16310	26476	3.06	1.9E-01	AF072724.1	NT	Zea mays starch branching enzyme I (sbe1) gene, complete cds
6658	16538	26735	1.62	1.9E-01	AL161557.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 57
7041	16918	27109	12.89	1.9E-01	AB033024.1	NT	Homo sapiens mRNA for KIAA1198 protein, partial cds
8038	17930	28176	2.16	1.9E-01	AL161503.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 15
8038	17930	28177	2.16	1.9E-01	AL161503.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 15
8137	18025	28271	1.75	1.9E-01	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
8961	18768	29060	2.61	1.9E-01	AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
9546	19146		1.67	1.9E-01	AF055900.1	NT	Drosophila melanogaster clathrin light chain mRNA, complete cds
9880	19546		1.26	1.9E-01	AF001168.1	NT	Arabidopsis thaliana receptor-like kinase LECRK1 (LECRK1) gene, complete cds
29	10016	19811	2.26	1.8E-01	U73200.1	NT	Mus musculus p116Rip mRNA, complete cds
260	12663	20041	1.22	1.8E-01	AB022090.1	NT	Mus musculus Cctg gene for chaperonin containing TOP-1 gamma subunit, partial cds
366	10322	20145	2.41	1.8E-01	4502532	NT	Homo sapiens calcium channel, voltage-dependent, beta 2 subunit (CACNB2) mRNA, and translated products
729	10661	20493	2.15	1.8E-01	AB021490.2	NT	Oryzias latipes gene for membrane guanylyl cyclase OIGC1, complete cds
966	10889	20735	0.85	1.8E-01	AI912212.1	EST_HUMAN	wd1102.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2337051 3'
1075	10990	20832	1.21	1.8E-01	AF000580.1	NT	Dicystelium discoideum plasmid Dqp5, complete genome
1267	11174	21024	5.28	1.8E-01	AL117189.1	NT	Yersinia pestis plasmid pCD1
1487	11392	21252	1.29	1.8E-01	6753947	NT	Mus musculus guanylate nucleotide binding protein 1 (Gbp1), mRNA
1487	11392	21253	1.29	1.8E-01	6753947	NT	Mus musculus guanylate nucleotide binding protein 1 (Gbp1), mRNA
1803	11700		0.92	1.8E-01	4505036	NT	Homo sapiens latent transforming growth factor beta binding protein 4 (LTBP4) mRNA
1823	11720		1.93	1.8E-01	AI733708.1	EST_HUMAN	qq22410.x5 NCL_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1761811 3' similar to TR:O756936 O756936 GAMMA BUTYROBETAINE HYDROXYLASE ;
1873	11769	21644	1.6	1.8E-01	AB051897.1	NT	Mus musculus Scya6, Scya9, Scya16-ps, Scya5 genes for small inducible cytokine A6 precursor, small inducible cytokine A9 precursor, Scya16 pseudogene, small inducible cytokine A5 precursor, complete cds
2660	12527		2.99	1.8E-01	AW935728.1	EST_HUMAN	QV3-DT0018-081299-036-g04 DT0018 Homo sapiens cDNA
2868	12796		1.61	1.8E-01	AF184589.1	NT	Jonopsidium acule LEAFY protein (LEAFY2) gene, partial cds
2873	12800	22595	1.09	1.8E-01	AW182300.1	EST_HUMAN	xj41a03.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2659756 3'
3085	13012	22803	1.28	1.8E-01	AW995178.1	EST_HUMAN	QV0-BN0041-070300-147-c04 BN0041 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3570	13484	23275	1.07	1.8E-01	H03369.1	EST_HUMAN	y45e01.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:151704 3' similar to contains Alu repetitive element
3570	13484	23276	1.07	1.8E-01	H03369.1	EST_HUMAN	y45e01.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:151704 3' similar to contains Alu repetitive element
4154	14054	23828	0.8	1.8E-01	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
4238	14137	23954.1	1.13	1.8E-01	D37954.1	NT	Bovine NB25 mRNA for MHC class II (BoLA-DQB), complete cds
4456	14350	24141	5.12	1.8E-01	AL161556.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 56
4663	14549	24339	2.36	1.8E-01	AB051897.1	NT	Mus musculus Scya6, Scya9, Scya16-ps, Scya5 genes for small inducible cytokine A6 precursor, small inducible cytokine A9 precursor, Scya16 pseudogene, small inducible cytokine A5 precursor, complete cds
4700	14586	24377	0.93	1.8E-01	X92179.1	NT	S.tuberosum mRNA for alcohol dehydrogenase
4977	14852	24618	1.77	1.8E-01	AW814270.1	EST_HUMAN	MR3-S10203-151299-112-g06 ST0203 Homo sapiens cDNA
5027	14900	24670	4.17	1.8E-01	AF181258.1	NT	Mesocricetus auratus Na-taurocholate cotransporting polypeptide mRNA, partial cds
5053	14925	24697	1.28	1.8E-01	AI439881.1	EST_HUMAN	t57e04.x1 NCL CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2134560 3'
5117	14985	25335	1.03	1.8E-01	AJ00742.1	NT	Homo Sapiens histH1 gene, 5' UTR
5549	15465	25535	1.41	1.8E-01	AL161594.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 90
5922	15827	25952	1.29	1.8E-01	Q9QY14	SWISSPROT	FORKHEAD BOX PROTEIN E3
5948	15853	25952	2.5	1.8E-01	N94853.1	EST_HUMAN	y62h02.r1 Soares multiple sclerosis 2NbhMSP Homo sapiens cDNA clone IMAGE:278163 5'
6179	16065	26214	1.38	1.8E-01	AB018561.1	NT	Citullus lanatus mRNA for wsus, complete cds
6179	16065	26215	1.38	1.8E-01	AB018561.1	NT	Citullus lanatus mRNA for wsus, complete cds
7382	17251	27456	1.72	1.8E-01	M73258.1	NT	Human cellular DNA/Human papillomavirus proviral DNA
7396	17314	27521	1.22	1.8E-01	9626232	NT	Bacteriophage Iike, complete genome
7933	17783	28022	1.19	1.8E-01	X63440.1	NT	M.musculus mRNA for P19-protein tyrosine phosphatase
8033	17925	28172	3.19	1.8E-01	X77336.1	NT	A.thaliana mRNA for ribonucleotide reductase R2
8065	17956	28205	6.65	1.8E-01	U39906.1	NT	Bacteriophage r11 integrase, repressor protein (rro), dUTPase, holin and lysin genes, complete cds
8118	16065	26214	2.9	1.8E-01	AB018561.1	NT	Citullus lanatus mRNA for wsus, complete cds
8118	16065	26215	2.9	1.8E-01	AB018561.1	NT	Citullus lanatus mRNA for wsus, complete cds
8119	18007	28254	3.88	1.8E-01	AF019107.1	NT	Dictyostelium discoideum unknown (DG1041) gene, complete cds
8381	18258	28507	2.64	1.8E-01	M59257.1	NT	Human carcinoembryonic antigen (CEA) gene, exon 4
8758	17907	28152	3.98	1.8E-01	X57033.1	NT	B.taurus mRNA for potassium channel
8976	18781	29073	2.83	1.8E-01	8394421	NT	Rattus norvegicus Thromboxane receptor (Tbx2r), mRNA
9169	18912	25344	1.65	1.8E-01	BF348623.1	EST_HUMAN	602019928F1 NCI CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4155318 5'
9625	19200		2.05	1.8E-01	Q96682	SWISSPROT	DNA TERMINAL PROTEIN (BELLETTI PROTEIN) (PTP PROTEIN)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9738	19272		7.94	1.8E-01	R24494.1	EST_HUMAN	YH48h10.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:133027 5'
9779	19294		1.63	1.8E-01	Y11114.1	NT	E. dispar mRNA for hexokinase (hpk1)
563	10503	20309	1.8	1.7E-01	BE385194.1	EST_HUMAN	601274604F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3615768 5'
788	10717	20559	2.04	1.7E-01	X53330.1	NT	P. dumerilii histone gene cluster for core histones H2A, H2B, H3 and H4
945	10870		1.89	1.7E-01	P35916	SWISSPROT	NEUROFILAMENT TRIPLET L PROTEIN (NEUROFILAMENT LIGHT POLYPEPTIDE) (NF-L)
1042	10960	20802	1.6	1.7E-01	AF081810.1	NT	Lymantria dispar nucleopolydnavirus, complete genome
1042	10960	20803	1.6	1.7E-01	AF081810.1	NT	Lymantria dispar nucleopolydnavirus, complete genome
1938	11833		3.8	1.7E-01	AF255051.1	NT	Homo sapiens BNIP3H (BNIP3H) gene, complete cds; nuclear gene for mitochondrial product
2829	12758	22548	1.93	1.7E-01	AF000716.1	NT	Vibrio cholerae hypoxanthine phosphoribosyltransferase (hpt) gene, partial cds, hemagglutinin/protease regulatory protein (hapR) gene, complete cds, and YRAL VIBCO gene, partial cds
2829	12758	22549	1.93	1.7E-01	AF000716.1	NT	Vibrio cholerae hypoxanthine phosphoribosyltransferase (hpt) gene, partial cds, hemagglutinin/protease regulatory protein (hapR) gene, complete cds, and YRAL VIBCO gene, partial cds
2896	12823	22616	1.74	1.7E-01	AA336909.1	EST_HUMAN	EST41651 Endometrial tumor Homo sapiens cDNA 5' end
2967	12894	22693	1.35	1.7E-01	AJ238736.1	NT	Naja naja atra ctk-1 gene, exons 1-3
2967	12894	22694	1.35	1.7E-01	AJ238736.1	NT	Naja naja atra ctk-1 gene, exons 1-3
3067	12994	22785	1.89	1.7E-01	AF081514.1	NT	Taxus canadensis geranylgeranyl diphosphate synthase mRNA, complete cds
3401	13318	23119	1.96	1.7E-01	AJ299505.1	NT	Anabaena sp. ORF4 (partial), ORF3, ORF2, ORF1, adpA gene, adpB gene, adpC gene, adpD gene, adpE gene and adpF gene
3557	13471	23282	1	1.7E-01	AJ224877.1	NT	Homo sapiens hap1 gene, complete CDS
3859	13770	23562	4.41	1.7E-01	AJ235377.1	NT	Homo sapiens derivative 11 breakpoint fragment: partial intron 10 of the ALL-1/MLL/HRX gene fused to intron 5 of the AF-4/FEL gene
4459	14353		1.88	1.7E-01	X52936.1	NT	Schistosoma gregaria alpha repetitive DNA
4732	14617	24403	1.4	1.7E-01	AJ247635.1	EST_HUMAN	qhs7e09.x1 Soares fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1848808 3' similar to contains ORF.b1 ORF repetitive element ;
4986	14861		1.16	1.7E-01	U28376.1	NT	Zea mays calcium-dependent protein kinase (MZECDPK2) mRNA, complete cds
5067	14937		1.18	1.7E-01	AF072725.1	NT	Zea mays starch branching enzyme 1b (ae) gene, complete cds
5321	15241	25046	1.76	1.7E-01	AA470686.1	EST_HUMAN	ne13a02.s1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:881066 3' similar to gb:M17886 60S ACIDIC RIBOSOMAL PROTEIN P1 (HUMAN);
5321	15241	25047	1.76	1.7E-01	AA470686.1	EST_HUMAN	ne13a02.s1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:881066 3' similar to gb:M17886 60S ACIDIC RIBOSOMAL PROTEIN P1 (HUMAN);
5820	15726	25839	12.31	1.7E-01	H72118.1	EST_HUMAN	ys02g06.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:213658 3'
6112	16006		2.15	1.7E-01	AF026552.3	NT	Mesocricetus auratus oviductin precursor (OVI) gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6320	18183	26344	7.96	1.7E-01	BE734179.1	EST_HUMAN	601569022F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3843964 5'
6588	16468	26658	1.2	1.7E-01	AF000573.1	NT	Homo sapiens homogenisate 1,2-dioxygenase gene, complete cds
6814	16693	26982	7.03	1.7E-01	7706426	NT	Homo sapiens cleavage and polyadenylation specificity factor 3, 73kD subunit (CPSF3), mRNA
6814	16693	26983	7.03	1.7E-01	7706426	NT	Homo sapiens cleavage and polyadenylation specificity factor 3, 73kD subunit (CPSF3), mRNA
7066	16943	27135	2.46	1.7E-01	D00384.1	NT	Rat (SHR strain) SX1 gene
7531	17382	27593	7.38	1.7E-01	AP001508.1	NT	Bacillus halodurans genomic DNA, section 2/14
7601	17452	27666	2.06	1.7E-01	U16288.1	NT	Human class IV alcohol dehydrogenase (ADH7) gene, exon 3
7875	17725		2.42	1.7E-01	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
7942	17792	28032	1.48	1.7E-01	11427203	NT	Homo sapiens solute carrier family 7 (cationic amino acid transporter, y+ system), member 2 (SLC7A2), mRNA
7943	17793	28033	1.57	1.7E-01	AA627972.1	EST_HUMAN	nc60e07.s1 NCL_CGAP_Co8 Homo sapiens cDNA clone IMAGE:1148292 3' similar to gb:L25081
8067	17958	28208	9.13	1.7E-01	BE390835.1	EST_HUMAN	TRANSFORMING PROTEIN RHOC (HUMAN);
8182	18068	28317	2.47	1.7E-01	AA814617.1	EST_HUMAN	601286547F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3613258 5'
8456	18329	28589	7.88	1.7E-01	7106300	NT	af43a03.s1 NCL_CGAP_CNS1 Homo sapiens cDNA clone IMAGE:1426924 3'
8456	18329	28590	7.88	1.7E-01	7106300	NT	Mus musculus adenomatosis polyposis coli binding protein Ebt1 (Ebt1), mRNA
8949	18757		1.92	1.7E-01	P15272	SWISSPROT	Mus musculus adenomatosis polyposis coli binding protein Ebt1 (Ebt1), mRNA
9012	18811	29107	4.38	1.7E-01	11418157	NT	AMP NUCLEOSIDASE
9139	19666		1.5	1.7E-01	AL163278.2	NT	Homo sapiens calcium channel, voltage-dependent, alpha 1I subunit (CACNA1I), mRNA
9420	19513		1.28	1.7E-01	A1824404.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C078
9705	19253	25218	5.79	1.7E-01	U01317.1	NT	tx69g05.x1 NCL_CGAP_Ur1 Homo sapiens cDNA clone IMAGE:2274872 3' similar to gb:M73779 RETINOIC ACID RECEPTOR ALPHA-1 (HUMAN);
120	10097	19917	1.88	1.6E-01	AF217632.1	NT	Human beta globin region on chromosome 11
664	12641	20416	1.53	1.6E-01	R31497.1	EST_HUMAN	Homo sapiens mevalonate kinase gene, exon 6 and 7
1505	11409	21268	4.05	1.6E-01	AF298117.1	NT	yh76f12.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:1355599 5'
1882	11778	21653	2.4	1.6E-01	P22063	SWISSPROT	Homo sapiens homeobox protein OTX2 gene, complete cds
1941	11836		1	1.6E-01	U10334.1	NT	AXONIN-1 PRECURSOR (AXONAL GLYCOPROTEIN TAG-1)
2335	12719	22115	0.96	1.6E-01	X94232.1	NT	Crassostrea gigas RNA polymerase II largest subunit mRNA, partial cds
2443	12320	22218	2.19	1.6E-01	AB037729.1	NT	H. sapiens mRNA for novel T-cell activation protein
2863	12791	22583	8.9	1.6E-01	AF185589.1	NT	Homo sapiens mRNA for KIAA1308 protein, partial cds
2863	12791	22584	8.9	1.6E-01	AF185589.1	NT	Homo sapiens cytochrome P450 3A4 (CYP3A4) gene, promoter region
3581	13495	23285	1.31	1.6E-01	AJ003165.1	NT	Homo sapiens cytochrome P450 3A4 (CYP3A4) gene, promoter region
3581	13495	23286	1.31	1.6E-01	AJ003165.1	NT	Populus trichocarpa cv. Trichobel ABI3 gene
3919	13828		2.61	1.6E-01	AE004413.1	NT	Populus trichocarpa cv. Trichobel ABI3 gene
							Vibrio cholerae chromosome II, section 70 of 93 of the complete chromosome

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4234	14132	23908	7.92	1.6E-01	AF179880.1	NT	Homo sapiens apelin gene, complete cds
4353	14249		2.44	1.6E-01	AW1968601.1	EST_HUMAN	EST380677 IMAGE resequences, MAGJ Homo sapiens cDNA
4361	14257		4.01	1.6E-01	8753319	NT	Mus musculus chaperonin subunit 3 (gamma) (Cct3), mRNA
4781	14665	24451	0.86	1.6E-01	Z28330.1	NT	S.cerevisiae chromosome XI reading frame ORF YKR105c
4781	14665	24452	0.86	1.6E-01	Z28330.1	NT	S.cerevisiae chromosome XI reading frame ORF YKR105c
4865	14745	24524	1.14	1.6E-01	AA088943.1	EST_HUMAN	z184h09.s1 Stragene colon (#837204) Homo sapiens cDNA clone IMAGE:511361 3' similar to TR:E221955
4869	14769	24546	1.92	1.6E-01	AJ006356.1	NT	E221955 38,855 BP SEGMENT OF CHROMOSOME XIV.;
4889	14769	24547	1.92	1.6E-01	AJ006356.1	NT	Lycopersicon esculentum RsaI fragment 2, satellite region
4958	14833	24601	1.09	1.6E-01	BE018707.1	EST_HUMAN	Lycopersicon esculentum RsaI fragment 2, satellite region
5390	15309	25162	3.12	1.6E-01	AW197496.1	EST_HUMAN	bb83h08.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3049023 5' similar to gb:M61715 TRYPTOPHANYL-TRNA SYNTHETASE (HUMAN); gb:X69657 M.musculus (MOUSE); xm43701.x1 NCI CGAP_GC6 Homo sapiens cDNA clone IMAGE:2886969 3' similar to TR:O75984 O75984 HYPOTHETICAL 127.6 KD PROTEIN ;
5390	15309	25163	3.12	1.6E-01	AW197496.1	EST_HUMAN	xm43701.x1 NCI CGAP_GC6 Homo sapiens cDNA clone IMAGE:2886969 3' similar to TR:O75984 O75984 HYPOTHETICAL 127.6 KD PROTEIN ;
5398	15317	25364	2.07	1.6E-01	AF034716.1	NT	Rattus norvegicus CCAA/Tenhancer binding protein epsilon (cbbpe) gene, complete cds
5873	15779	25998	2.24	1.6E-01	AL161588.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 84
5873	15779	25999	2.24	1.6E-01	AL161588.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 84
6157	15115	24858	3.7	1.6E-01	AW291215.1	EST_HUMAN	UI-H-B12-egl-b-06-0-UI.s1 NCI CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2724418 3'
6571	16429	26612	1.84	1.6E-01	AW246359.1	EST_HUMAN	2822248.5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822248 5'
6592	16472	26662	1.42	1.6E-01	L49349.1	NT	Gorilla gorilla androgen receptor gene, partial exon
7187	17064	27254	1.89	1.6E-01	Z49501.1	NT	S.cerevisiae chromosome X reading frame ORF YJR001w
7564	17415		1.7	1.6E-01	BF375171.1	EST_HUMAN	RC3-ST0200-047199-017-h01 ST0200 Homo sapiens cDNA
7565	17416	27631	1.91	1.6E-01	Z49501.1	NT	S.cerevisiae chromosome X reading frame ORF YJR001w
8049	17940	28190	2.71	1.6E-01	AW850853.1	EST_HUMAN	IL3-CT0220-11199-028-G01 CT0220 Homo sapiens cDNA
8364	18241	28490	1.78	1.6E-01	O14647	SWISSPROT	CHROMODOMAIN-HELICASE-DNA-BINDING PROTEIN 2 (CHD-2)
8364	18241	28491	1.78	1.6E-01	O14647	SWISSPROT	CHROMODOMAIN-HELICASE-DNA-BINDING PROTEIN 2 (CHD-2)
8459	18332		7.6	1.6E-01	AF106064.1	NT	Plasmodium falciparum calcium-dependent protein kinase-3 (cdpk3) gene, complete cds
8713	18530	28814	10.07	1.6E-01	6671552	NT	Mus musculus adaptor-related protein complex AP-1, beta 1 subunit (Apt1b1), mRNA
9001	18804	29097	2.69	1.6E-01	AW871727.1	EST_HUMAN	QV2-PT0010-160400-133-a08 PT0010 Homo sapiens cDNA
9025	19678		2.17	1.6E-01	6679466	NT	Mus musculus protein kinase, cGMP-dependent, type II (Prkg2), mRNA
9141	18896	28795	2.33	1.6E-01	AV719885.1	EST_HUMAN	AV719885 GLC Homo sapiens cDNA clone GLCEMF07 5'
9565	19493		6.33	1.6E-01	AB045310.1	NT	Cucumis sativus KS mRNA for ent-kaurene synthase, complete cds
9727	19265		2.84	1.6E-01	AK024496.1	NT	Homo sapiens mRNA for FLJ00104 protein, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9807	19319		2.47	1.5E-01	AF287344.1	NT	Fuchsia hybrid cultivar Qiu 94208 ribosomal protein S10 gene, partial cds; nuclear gene for mitochondrial product
9827	19328	25208	1.27	1.5E-01	9506522	NT	Rattus norvegicus chondroitin sulfate proteoglycan 5 (neuroglycan C) (Cspg5), mRNA
248	10214	20030	1.87	1.5E-01	BE710087.1	EST_HUMAN	IL3-HT0619-040700-197-E05 HT0619 Homo sapiens cDNA
248	10214	20031	1.87	1.5E-01	BE710087.1	EST_HUMAN	IL3-HT0619-040700-197-E05 HT0619 Homo sapiens cDNA
572	12640		2.28	1.5E-01	AV711696.1	EST_HUMAN	AV711696 DCA Homo sapiens cDNA clone DCAADH06 5'
766	10697	20534	1.4	1.5E-01	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
1076	10992	20834	0.88	1.5E-01	AJ009735.1	NT	Cyprinus carpio mRNA for EGGS22 myosin heavy chain, 3'UTR
1081	10997	20838	1.87	1.5E-01	AJ251885.1	NT	Homo sapiens partial SLC22A2 gene for organic cation transporter (OCT2), exon 1
1097	11013		1.82	1.5E-01	L36125.1	NT	Rattus norvegicus insulin-responsive glucose transporter (GLUT4) gene, 5' end
1198	11108	20953	1.36	1.5E-01	AW195516.1	EST_HUMAN	xn39a11.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2696085 3'
1254	11161	21010	2.81	1.5E-01	D26535.1	NT	Human gene for dihydrolipoamide succinyltransferase, complete cds (exon 1-15)
1254	11161	21011	2.81	1.5E-01	D26535.1	NT	Human gene for dihydrolipoamide succinyltransferase, complete cds (exon 1-15)
1466	11371	21238	1.49	1.5E-01	AF117340.1	NT	Mus musculus MAP kinase kinase kinase 1 (Mekkt1) mRNA, complete cds
1866	11762	21636	1.54	1.5E-01	AW444451.1	EST_HUMAN	UH-H-B13-akb-b-09-0-JL.s1 NCL_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2733641 3'
2679	12544	22435	1.12	1.5E-01	BF695381.1	EST_HUMAN	602083269F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4247537 5'
2999	12927	22719	0.89	1.5E-01	M81441.1	NT	Bos taurus factor V variant 2 (factor V) mRNA, complete cds
3308	13229	23034	4.22	1.5E-01	AA935049.1	EST_HUMAN	oo68405.s1 NCL_CGAP_GC4 Homo sapiens cDNA clone IMAGE:1571337 3' similar to gb:M11433
3322	13242	23048	0.87	1.5E-01	Z33104.1	NT	RETINOL-BINDING PROTEIN I, CELLULAR (HUMAN);
3322	13242	23049	0.87	1.5E-01	Z33104.1	NT	L. stagnalis mRNA for G protein-coupled receptor
						NT	L. stagnalis mRNA for G protein-coupled receptor
3380	13298	23097	0.96	1.5E-01	AW612237.1	EST_HUMAN	hh29f02.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2956539 3' similar to contains element MER16 repetitive element ;
3696	13610	23394	1.34	1.5E-01	U09964.1	NT	Mus musculus ICR/Swiss glycerinaldehyde 3-phosphate dehydrogenase (Gapd-S) gene, complete cds
3706	13619	23403	185.26	1.5E-01	7108358	NT	Homo sapiens pyruvate dehydrogenase kinase, isoenzyme 1 (PDK1), nuclear gene encoding mitochondrial protein, mRNA
3791	13703	23490	2.35	1.5E-01	AW665963.1	EST_HUMAN	hj10f06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2981411 3'
3806	13718	23506	0.8	1.5E-01	AJ003165.1	NT	Populus trichocarpa cv. Trichobal ABI3 gene
3806	13718	23507	0.8	1.5E-01	AJ003165.1	NT	Populus trichocarpa cv. Trichobal ABI3 gene
3964	13871	23649	0.96	1.5E-01	AW366659.1	EST_HUMAN	RC2-HT0149-197099-012-c09 HT0149 Homo sapiens cDNA
4006	13912	23687	0.97	1.5E-01	Z12628.1	NT	B. napus mitochondrial DNA for ORF198
4091	13991	23768	8.36	1.5E-01	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
4623	14511	24301	1.34	1.5E-01	BF687665.1	EST_HUMAN	602087192F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4066223 5'

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4645	12544	22435	2.18	1.5E-01	BF695381.1	EST_HUMAN	602083269F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4247537 5'
4680	14566	24361	1.08	1.5E-01	BE173796.1	EST_HUMAN	CM0-HT0565-280200-245-b10 HT0565 Homo sapiens cDNA
4680	14566	24362	1.08	1.5E-01	BE173796.1	EST_HUMAN	CM0-HT0565-280200-245-b10 HT0565 Homo sapiens cDNA
4929	14808	24576	1.3	1.5E-01	AL161560.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 60
5072	14942	24716	0.94	1.5E-01	AF003105.1	NT	Arabidopsis thaliana AP2 domain containing protein RAP2.12 mRNA, partial cds
5216	15139	24833	2.02	1.5E-01	P07996	SWISSPROT	THROMBOSPONDIN 1 PRECURSOR
5266	15188		5.67	1.5E-01	P15196	SWISSPROT	SEX HORMONE-BINDING GLOBULIN PRECURSOR (SHBG) (SEX STEROID-BINDING PROTEIN) (SBP) (TESTIS-SPECIFIC ANDROGEN-BINDING PROTEIN) (ABP)
5400	15319	25367	4.06	1.5E-01	AW850754.1	EST_HUMAN	IL3-CT0219-160200-064-F10 CT0219 Homo sapiens cDNA
5424	15345	25398	6.77	1.5E-01	U65016.1	NT	Mus musculus transforming growth factor alpha (TGFA) mRNA, complete cds
5424	15345	25399	6.77	1.5E-01	U65016.1	NT	Mus musculus transforming growth factor alpha (TGFA) mRNA, complete cds
5652	15564	25660	1.9	1.5E-01	6753659	NT	Mus musculus DNA methyltransferase 2 (Dnmt2) mRNA
5652	15564	25661	1.9	1.5E-01	6753659	NT	Mus musculus DNA methyltransferase 2 (Dnmt2) mRNA
5684	15593	25694	1.87	1.5E-01	AJ276505.1	NT	Mus musculus genomic fragment, 279 Kb, chromosome 7
5760	15688	25774	2.44	1.5E-01	BE727658.1	EST_HUMAN	601564322F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3833981 5'
5785	15691		1.66	1.5E-01	4506396	NT	Homo sapiens RAD54 (S.cerevisiae)-like (RAD54L) mRNA
5828	15734	25845	1.78	1.5E-01	AF134907.1	NT	Influenza B virus (B/Nanchang/480/94) NB protein gene, complete cds; and neuraminidase gene, partial cds
5917	19455	25948	1.96	1.5E-01	AE001039.1	NT	Archaeoglobus fulgidus section 88 of 172 of the complete genome
5935	15840	25963	5.13	1.5E-01	11417236	NT	Homo sapiens chromosome 5 open reading frame 3 (C5ORF3), mRNA
5942	15847	25971	1.81	1.5E-01	P48508	SWISSPROT	GLUTAMATE-CYSTEINE LIGASE REGULATORY SUBUNIT (GAMMA-GLUTAMYL-CYSTEINE SYNTHETASE) (GAMMA-ECS) (GCS LIGHT CHAIN)
5972	15876	26000	2.09	1.5E-01	Q28462	SWISSPROT	AMELOGENIN
6031	15935	26067	1.4	1.5E-01	P30143	SWISSPROT	HYPOTHETICAL 51.7 KD PROTEIN IN THRC-TALB INTERGENIC REGION (ORF8)
6166	15123	24866	5.63	1.5E-01	AW970295.1	EST_HUMAN	EST382376 IMAGE resequences, MAGK Homo sapiens cDNA
6284	16148		1.77	1.5E-01	AF210842.1	NT	Homo sapiens HARP (HARP) gene, exon 17 and complete cds
6374	16236	26396	1.88	1.5E-01	AI973157.1	EST_HUMAN	wr52c08.x1 NCJ CGAP_UH1 Homo sapiens cDNA clone IMAGE:2491310 3'
6481	16340	26507	1.68	1.5E-01	AW500611.1	EST_HUMAN	UI-HF-BNO-akk-d-05-0-UI-r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077409 5'
6481	16340	26508	1.68	1.5E-01	AW500611.1	EST_HUMAN	UI-HF-BNO-akk-d-05-0-UI-r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077409 5'
6786	16665	26856	1.22	1.5E-01	AA970317.1	EST_HUMAN	oo85g12.s1 NCJ CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1573030 3' similar to gb:M26062
6895	16774		11.77	1.5E-01	C16900.1	EST_HUMAN	INTERLEUKIN-2 RECEPTOR BETA CHAIN PRECURSOR (HUMAN);
6912	16790	26983	1.88	1.5E-01	L27835.1	NT	C16800 Clontech human aorta polyA+ mRNA (#6572) Homo sapiens cDNA clone GEN-529H09 5'
6996	16873	27064	1.44	1.5E-01	D84476.1	NT	Pangasinanodon gigas growth hormone (GH) mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7130	17007	27200	1.71	1.5E-01	4501972	NT	Homo sapiens adaptor-related protein complex 1, beta 1 subunit (ADTB1), mRNA
7265	17142	27335	2.48	1.5E-01	N74226.1	EST_HUMAN	zaf5e06.s1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:296866 3' similar to PIR:S44443 S44443 RAD23 protein homolog2 - human ;
7306	17182		2.98	1.5E-01	AV754819.1	EST_HUMAN	AV754819 TP Homo sapiens cDNA clone TPAAHB12 5'
7438	16451	26641	6.6	1.5E-01	U00455.1	NT	Acipenser transmontano vitellogenin mRNA, partial cds
7706	17556	27781	7.02	1.5E-01	AF007570.1	NT	Aplysia californica carboxypeptidase D mRNA, complete cds
7706	17556	27782	7.02	1.5E-01	AF007570.1	NT	Aplysia californica carboxypeptidase D mRNA, complete cds
7860	17710	27955	2.86	1.5E-01	X98852.1	NT	P. leiusculus mRNA for integrin beta subunit
7908	17758	27998	2.45	1.5E-01	AI814046.1	EST_HUMAN	wk53h12.x1 NCL CGAP_P122 Homo sapiens cDNA clone IMAGE:2419175 3' similar to gb:M27508 BETA GALACTOSIDASE-RELATED PROTEIN PRECURSOR (HUMAN);
7908	17758	27999	2.45	1.5E-01	AI814046.1	EST_HUMAN	wk53h12.x1 NCL CGAP_P122 Homo sapiens cDNA clone IMAGE:2419175 3' similar to gb:M27508 BETA GALACTOSIDASE-RELATED PROTEIN PRECURSOR (HUMAN);
7939	17789	28031	1.54	1.5E-01	U40932.1	NT	Danio rerio transcription factor Pax9b (Pax9) mRNA, complete cds
8009	17859	28103	1.35	1.5E-01	AJ011964.1	NT	Claviceps purpurea ps1 gene
8009	17859	28104	1.35	1.5E-01	AJ011964.1	NT	Claviceps purpurea ps1 gene
8199	18084	28334	5.15	1.5E-01	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
8199	18084	28335	5.15	1.5E-01	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
8342	18219		1.74	1.5E-01	AB042975.1	NT	Sus scrofa CYP51 gene for lanosterol 14 alpha-demethylase, exon 1
8425	18299	28555	1.73	1.5E-01	AW841915.1	EST_HUMAN	IL5-CN0024-030300-025-D04 CN0024 Homo sapiens cDNA
8506	16236	26396	2.17	1.5E-01	AI973157.1	EST_HUMAN	wr52c08.x1 NCL CGAP_U11 Homo sapiens cDNA clone IMAGE:2491310 3'
9099	19547		20.02	1.5E-01	BF700582.1	EST_HUMAN	602128753F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285549 5'
9531	19565		4.14	1.5E-01	R83077.1	EST_HUMAN	yp87e04.r1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:194430 5'
9621	19588		2.14	1.5E-01	AV741272.1	EST_HUMAN	AV741272 CB Homo sapiens cDNA clone CBDA04 5'
9726	19497	25133	3.99	1.5E-01	AL139074.2	NT	Campylobacter jejuni NCTC11168 complete genome; segment 1/6
9932	19402	25179	3.01	1.5E-01	AJ276242.1	NT	Sus scrofa mRNA for sodium iodide symporter
9972	19432		1.58	1.5E-01	AF020346.1	NT	Rattus norvegicus pyridoxal kinase mRNA, complete cds
296	10260		1.96	1.4E-01	AF009663.1	NT	Homo sapiens T cell receptor beta locus, TCRBV8S5P to TCRBV21S2A2 region
892	10818		2.57	1.4E-01	ID78638.1	NT	Xenopus laevis mRNA for DNA (cytosine-5)-methyltransferase, complete cds
1238	11145		1.62	1.4E-01	T91864.1	EST_HUMAN	yd54c01.s1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:112032 3'
1714	11615		1.43	1.4E-01	6679980	NT	Mus musculus growth differentiation factor 5 (Gdf5), mRNA
1717	11618	21487	1.53	1.4E-01	AE001710.1	NT	Thermotoga maritima section 22 of 136 of the complete genome
1863	11759		0.94	1.4E-01	AW135741.1	EST_HUMAN	UI-H-B11-acf-a-09-0-UJ.s1 NCL CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2714009 3'
1942	11837		10.35	1.4E-01	AA720615.1	EST_HUMAN	mv72d07.s1 NCL CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1283821 3'
2426	12303	22199	0.97	1.4E-01	P30706	SWISSPROT	GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE PRECURSOR (GPAT)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2762	12624	22517	3.07	1.4E-01	AI933496.1	EST_HUMAN	wm74d01.x1 NCI_CGAP_U2 Homo sapiens cDNA clone IMAGE:2441665 3'
3823	13735	23524	1	1.4E-01	R59232.1	EST_HUMAN	y97a03.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:41467 5'
3823	13735	23525	1	1.4E-01	R59232.1	EST_HUMAN	y97a03.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:41467 5'
4083	13985	23762	8.38	1.4E-01	AI699094.1	EST_HUMAN	b56c02.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2273570 3'
4083	13985	23763	8.38	1.4E-01	AI699094.1	EST_HUMAN	b56c02.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2273570 3'
4144	14044	23817	3.16	1.4E-01	AE001710.1	NT	Thermotoga maritima section 22 of 136 of the complete genome
							zj50b01.s1 Soares_fetal_liver_inFLS_S1 Homo sapiens cDNA clone IMAGE:453673 3' similar to gb:X01057_rna1 INTERLEUKIN-2 RECEPTOR ALPHA CHAIN PRECURSOR (HUMAN); contains Alu repetitive element;
4313	14210		0.8	1.4E-01	AA776287.1	EST_HUMAN	QV3-SN0022-100500-186-h09 SN0022 Homo sapiens cDNA
5032	14904		0.91	1.4E-01	AW866022.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C084
5116	14984	24759	1	1.4E-01	AL163284.2	NT	Lycopodium obscurum genomic RAPD band 26
5147	15014	24784	0.81	1.4E-01	AJ005180.1	NT	ye15c11.s1 Stratiogene lung (#937210) Homo sapiens cDNA clone IMAGE:117812 3'
5248	15171	24944	4.5	1.4E-01	T90677.1	EST_HUMAN	Candida tropicalis DNA for mitochondrial NADP-linked isocitrate dehydrogenase, complete cds
5267	15189	24963	4.29	1.4E-01	AB004556.1	NT	Candida tropicalis DNA for mitochondrial NADP-linked isocitrate dehydrogenase, complete cds
5267	15189	24964	4.29	1.4E-01	AB004556.1	NT	hr67c02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3133538 3'
5805	15710	25823	2.72	1.4E-01	BE326891.1	EST_HUMAN	AU117147 HEMBA1 Homo sapiens cDNA clone HEMBA1000769 5'
5903	15809	25934	5.64	1.4E-01	AU117147.1	EST_HUMAN	AU117147 HEMBA1 Homo sapiens cDNA clone HEMBA1000769 5'
5903	15809	25935	5.64	1.4E-01	AU117147.1	EST_HUMAN	xb71a12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2581751 3'
5958	15863	25985	3.07	1.4E-01	AW082796.1	EST_HUMAN	601193523F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3537581 5'
5969	15874		1.56	1.4E-01	BE266536.1	EST_HUMAN	QV1-UM0036-080300-103-d09 UM0036 Homo sapiens cDNA
5982	15887	26009	1.89	1.4E-01	BF378533.1	EST_HUMAN	UI-H-B10-aat-c-09-0-U1.s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2710289 3'
6371	16233		1.62	1.4E-01	AW015373.1	EST_HUMAN	AV659047 GLC Homo sapiens cDNA clone GLCFSH06 3'
6936	16814		1.33	1.4E-01	AV659047.1	EST_HUMAN	EST179192 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end
7167	17044	27236	4.48	1.4E-01	AA307073.1	EST_HUMAN	601895465F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4124824 5'
7300	17176	27377	8.05	1.4E-01	BF310959.1	EST_HUMAN	z094a04.r1 Soares_fetal_heart_NbH19W Homo sapiens cDNA clone IMAGE:357102 5' similar to contains element KER repetitive element;
7343	17211	27410	1.36	1.4E-01	W93411.1	EST_HUMAN	Homo sapiens PHEX gene
7387	17256	27461	1.56	1.4E-01	Y10196.1	NT	Homo sapiens PHEX gene
7387	17256	27462	1.56	1.4E-01	Y10196.1	NT	Homo sapiens PHEX gene
7436	16449	26639	2.03	1.4E-01	AF121361.1	NT	Drosophila melanogaster signal transducing adaptor protein (STAM), serine threonine kinase lat (IAL), and zinc finger protein (DNZ1) genes, complete cds
8091	17982		2.02	1.4E-01	AA811480.1	EST_HUMAN	cg9a03.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1320364 3'
8216	18100	28352	3.28	1.4E-01	R53400.1	EST_HUMAN	y70c05.r1 Soares breast 2NBH19W Homo sapiens cDNA clone IMAGE:154088 5'
8613	18480	28751	1.89	1.4E-01	X66092.1	NT	C.perfringens ORF for putative membrane transport protein

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8764	17913	28158	2.23	1.4E-01	U28760.1	NT	Borrelia burgdorferi glyceraldehyde-3-phosphate dehydrogenase (GAPDH), phosphoglycerate kinase (PGK), triosephosphate isomerase (TPI) genes, complete cds
8813	18626		3.02	1.4E-01	X52102.1	NT	M.musculus p16K gene for 16 kDa protein
9365	19517	25138	1.48	1.4E-01	AB000890.1	NT	Ephydalia fluviatilis mRNA for aldolase, partial cds
9413	19065	25277	2.32	1.4E-01	X74773.1	NT	P.salina plastid gene secY
9427	19073		1.89	1.4E-01	11968117	NT	Rattus norvegicus desmin (Des), mRNA
9470	19734		1.82	1.4E-01	BE513802.1	EST_HUMAN	601315638F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3634329 5'
9560	19156		3.01	1.4E-01	AF083221.1	NT	Fugu rubripes putative neurotransmitter receptors, YDR140w homolog, and glycineamide ribonucleotide transferase (GART) genes, complete cds
9573	19163		2.29	1.4E-01	D64004.1	NT	Synechocystis sp. PCC6803 complete genome, 23/27, 2868767-3002965
9646	19754		3.28	1.4E-01	P10447	SWISSPROT	TYROSINE-PROTEIN KINASE TRANSFORMING PROTEIN ABL
9762	19282		1.41	1.4E-01	BE782738.1	EST_HUMAN	601465575F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3868795 5'
9831	19332		1.42	1.4E-01	11425031	NT	Homo sapiens ephrin-B3 (EFNB3), mRNA
9850	19566		3.41	1.4E-01	D82988.1	NT	Mus musculus mRNA for prolidase, complete cds
9926	19398		1.77	1.4E-01	AW377998.1	EST_HUMAN	MR0-HT0208-221299-204-c08 HT0208 Homo sapiens cDNA
319	10281	20098	2.69	1.3E-01	4758467	NT	Homo sapiens G protein-coupled receptor 50 (GPR50) mRNA
319	10281	20099	2.69	1.3E-01	4758467	NT	Homo sapiens G protein-coupled receptor 50 (GPR50) mRNA
518	10460	20271	1.86	1.3E-01	AB013139.1	NT	Homo sapiens gene for NBS1, complete cds
620	10557	20369	0.89	1.3E-01	AJ277606.1	NT	Human calicivirus HU/NLV/Girlington/93/UK RNA for capsid protein (ORF2), strain HU/NLV/Girlington/93/UK
620	10557	20370	0.89	1.3E-01	AJ277606.1	NT	Human calicivirus HU/NLV/Girlington/93/UK RNA for capsid protein (ORF2), strain HU/NLV/Girlington/93/UK
826	10753	20603	1.09	1.3E-01	X53330.1	NT	P.lumerillii histone gene cluster for core histones H2A, H2B, H3 and H4
876	10802	20652	1.83	1.3E-01	AF139518.1	NT	Rattus norvegicus A-kinase anchor protein mRNA, complete cds
1010	10928	20771	1.55	1.3E-01	AL117078.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
1111	11026		2.23	1.3E-01	AL115265.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
1197	11107	20952	1.07	1.3E-01	AV712467.1	EST_HUMAN	AV712467 DCA Homo sapiens cDNA clone DCAAFF05 5'
1426	11331		1.36	1.3E-01	AF146277.1	NT	Homo sapiens adapter protein CMS mRNA, complete cds
1916	11811	21689	2.56	1.3E-01	AL117078.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
2124	12012		1.29	1.3E-01	AJ243578.1	NT	Rhodospseudomonas acidiphila pucB5, pucA5, pucB6, pucA6, pucB7, pucA7, pucB8, pucA8 and pucC genes and ORF151
2245	12129		1.17	1.3E-01	AW812104.1	EST_HUMAN	RC4-ST0173-191099-032-d12 ST0173 Homo sapiens cDNA
2329	12210		2.99	1.3E-01	AE001016.1	NT	Archaeoglobus fulgidus section 91 of 172 of the complete genome
2542	12416	22306	3.49	1.3E-01	M86918.1	NT	Carassius auratus keratin type I mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3404	13321	23122	0.95	1.3E-01	M21572.1	NT	Bovine branched chain alpha-keto acid dihydrolipoyl transacylase mRNA, complete cds
3661	13575	23362	1.18	1.3E-01	AP000001.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1-287000 nt. position (117)
3661	13575	23363	1.18	1.3E-01	AP000001.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1-287000 nt. position (117)
3667	13581	23368	0.78	1.3E-01	AB032159.1	NT	Homo sapiens DD4 gene for dihydrolipoyl dehydrogenase 4 [AKR1C4], exon 2
3714	13575	23362	0.86	1.3E-01	AP000001.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1-287000 nt. position (117)
3714	13575	23363	0.86	1.3E-01	AP000001.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1-287000 nt. position (117)
3734	13646	23431	0.85	1.3E-01	6978940	NT	Rattus norvegicus Fibrinogen, gamma polypeptide (Fgg), mRNA
3906	13816		1.7	1.3E-01	AL161581.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 77
4046	13948		1.15	1.3E-01	AF020713.1	NT	Bacteriophage SPBc2 complete genome
4066	13968		3.44	1.3E-01	AW364341.1	EST_HUMAN	QV3-DT0018-081299-036-a03 DT0018 Homo sapiens cDNA
4075	13977	23756	1.89	1.3E-01	AF026805.1	NT	Schistosoma mansoni fructose biphosphate aldolase mRNA, complete cds
4093	13993	23770	16.36	1.3E-01	AW273741.1	EST_HUMAN	xv23f10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2813995 3'
4192	14092	23870	0.85	1.3E-01	AV752279.1	EST_HUMAN	AV752279 NPD Homo sapiens cDNA clone NPDAZE02 5'
4192	14092	23871	0.85	1.3E-01	AV752279.1	EST_HUMAN	AV752279 NPD Homo sapiens cDNA clone NPDAZE02 5'
4218	14116		1.65	1.3E-01	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
4433	14328	24116	2.16	1.3E-01	BE272339.1	EST_HUMAN	601126096F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:2990063 5'
4525	14418	24202	0.81	1.3E-01	BF679654.1	EST_HUMAN	602154306F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4295544 5'
4771	15075		3.17	1.3E-01	BE884017.1	EST_HUMAN	601510347F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3911987 5'
4903	14783		0.86	1.3E-01	AU136619.1	EST_HUMAN	AU136619 PLACE1 Homo sapiens cDNA clone PLACE1004693 5'
5074	14944	24718	1.21	1.3E-01	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
5074	14944	24719	1.21	1.3E-01	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
5173	15039	24805	0.9	1.3E-01	BF679819.1	EST_HUMAN	602154401F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4295305 5'
5173	15039	24806	0.9	1.3E-01	BF679819.1	EST_HUMAN	602154401F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4295305 5'
5292	15213	25013	2.51	1.3E-01	AW804417.1	EST_HUMAN	QV0-UM0093-100400-189-a06 UM0093 Homo sapiens cDNA
5428	15348		1.79	1.3E-01	AF056880.1	NT	Hepatitis C virus 68_CL10 genome polyprotein gene, partial cds
5904	15810	25936	13.21	1.3E-01	AB031326.1	NT	Schizosaccharomyces pombe gene for Alp41, complete cds
5956	15861	25983	2.04	1.3E-01	X89891.1	NT	C. jacchus intron 4 of visual pigment gene (red allele)
6305	16169		2	1.3E-01	H48664.1	EST_HUMAN	yr33d02.1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:207075 5'
6649	16529	26723	1.34	1.3E-01	11423294	NT	Homo sapiens PRO0611 protein (PRO0611), mRNA
6668	16548	26744	1.28	1.3E-01	BF690322.1	EST_HUMAN	602187015T1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4296074 3'
6858	16737		4.54	1.3E-01	Z74102.1	NT	S.cerevisiae chromosome IV reading frame ORF YDL054c
6886	16765		4.14	1.3E-01	89233919	NT	Homo sapiens core histone macroH2A2.2 (MACROH2A2), mRNA
6960	16838	27031	1.27	1.3E-01	BF690322.1	EST_HUMAN	602187015T1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4296074 3'
7452	17261	27467	4.45	1.3E-01	AF023129.1	NT	Oryctolagus cuniculus Ht,K+-ATPase alpha 2c subunit mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8029	17921		2.88	1.3E-01	BF330999.1	EST_HUMAN	MR4-BT0358-130700-010-h08 BT0358 Homo sapiens cDNA
8444	18318	28577	1.83	1.3E-01	AF119117.1	NT	Homo sapiens dopamine transporter (SLC6A3) gene, complete cds
8576	18444		5.13	1.3E-01	6671745	NT	Mus musculus cofilin 2, muscle (Gf2), mRNA
8873	18685	28976	3.72	1.3E-01	BE279449.1	EST_HUMAN	601158052F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3504804 5'
9261	18666	25320	1.97	1.3E-01	BE618346.1	EST_HUMAN	601462741F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866003 5'
9399	19054		3.18	1.3E-01	AJ242790.1	NT	Gallus gallus scyc1 gene for lymphotactin, exons 1-3
9757	19279		1.56	1.3E-01	AB026829.1	NT	Ephydraia fluviatilis mRNA for sALK-6, complete cds
							wu24d09.x1 Soares Dieckgraebe_colon_NHCD Homo sapiens cDNA clone IMAGE:2520977 3' similar to
9784	19297		1.32	1.3E-01	AW001114.1	EST_HUMAN	TR:O60287 O60287 KIAA0539 PROTEIN. ;
9945	19414		1.26	1.3E-01	BF571764.1	EST_HUMAN	602078440F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4253049 5'
							f39b02.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2098539 3' similar to gb:U05760_rna1
378	10362	20185	7.21	1.2E-01	AI421744.1	EST_HUMAN	ANNEXIN V (HUMAN);
418	9985		1.55	1.2E-01	U66912.1	NT	Dictyostelium discoideum ORF DG1016 gene, partial cds
535	10476		2.63	1.2E-01	AF039442.1	NT	Homo sapiens colon cancer antigen NY-CO-45 mRNA, partial cds
1355	11261	21117	2.78	1.2E-01	AU149146.1	EST_HUMAN	AU149146 NT2RM4 Homo sapiens cDNA clone NT2RM4001691 3'
1355	11261	21118	2.78	1.2E-01	AU149146.1	EST_HUMAN	AU149146 NT2RM4 Homo sapiens cDNA clone NT2RM4001691 3'
1361	11267		3.94	1.2E-01	AV735249.1	EST_HUMAN	AV735249 cda Homo sapiens cDNA clone cdaAJB11 5'
1490	11395		1.13	1.2E-01	AA897474.1	EST_HUMAN	al48e09.s1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1460584 3' similar to TR:Q16671
							Q16671 ANTI-MULLERIAN HORMONE TYPE II RECEPTOR PRECURSOR. ;
1613	11517	21377	1.17	1.2E-01	Q14934	SWISSPROT	NUCLEAR FACTOR OF ACTIVATED T-CELLS, CYTOPLASMIC 4 (T CELL TRANSCRIPTION FACTOR
1631	11535	21396	2.62	1.2E-01	AI285402.1	EST_HUMAN	NFAT3) (NF-ATC4) (NF-AT3)
1730	11631		29.48	1.2E-01	X89211.1	NT	q69f09.x1 NCI_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:1960553 3'
1877	11773		1.43	1.2E-01	AW449388.1	EST_HUMAN	H.sapiens DNA for endogenous retroviral like element
2134	12022	21919	2.1	1.2E-01	BF248490.1	EST_HUMAN	U1H-B13-aki-e-10-0-UI.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2734554 3'
2240	12124	22025	1.01	1.2E-01	AL163213.2	NT	601821567F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4046224 5'
2546	12420	22310	2.02	1.2E-01	AW996556.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C013
							QV3-BN0046-220300-129-f10 BN0046 Homo sapiens cDNA
							ts18g07.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2228988 3' similar to TR:Q14048 Q14048
2697	12561	22451	0.86	1.2E-01	A1623388.1	EST_HUMAN	COLLAGEN VI ALPHA-2 ALTERNATIVE C-TERMINAL DOMAIN. [1] ;contains element PTR5 repetitive
2812	12741	22637	1.5	1.2E-01	U18018.1	NT	element ;
							Human E1A enhancer binding protein (E1A-F) mRNA, partial cds
2872	12799	22694	1.96	1.2E-01	A1720470.1	EST_HUMAN	as80c09.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2335024 3' similar to gb:L05095
2904	12831	22628	2.89	1.2E-01	M16364.1	NT	60S RIBOSOMAL PROTEIN L30 (HUMAN);
							Human creatine kinase-B mRNA, complete cds

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Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2974	12901	22700	0.98	1.2E-01	X56882.1	NT	Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA)
3192	13117	22823	2	1.2E-01	AW370688.1	EST_HUMAN	QV1-BT0259-261099-021-405 BT0259 Homo sapiens cDNA
3219	13143		0.97	1.2E-01	U67600.1	NT	Methanococcus jannaschii section 142 of 150 of the complete genome
3433	13350		0.79	1.2E-01	Z99118.1	NT	Bacillus subtilis complete genome (section 15 of 21): from 2795131 to 3013540
3477	13393	23198	1.14	1.2E-01	X56882.1	NT	Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA)
3477	13393	23199	1.14	1.2E-01	X56882.1	NT	Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA)
3554	13350		1.2	1.2E-01	Z99118.1	NT	Bacillus subtilis complete genome (section 15 of 21): from 2795131 to 3013540
3704	13617		0.88	1.2E-01	BF128551.1	EST_HUMAN	601810786R1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4053668 3'
4090	13990	23766	2.2	1.2E-01	Z54255.1	NT	P.clarkii mRNA; repeat region (ID 2MRT7)
4090	13990	23767	2.2	1.2E-01	Z54255.1	NT	P.clarkii mRNA; repeat region (ID 2MRT7)
5012	14886		1.04	1.2E-01	P16466	SWISSPROT	HEMOLYSIN PRECURSOR
5174	15040	24807	1.47	1.2E-01	Q10441	SWISSPROT	HYPOTHETICAL 52.4 KD PROTEIN C12B10.08C IN CHROMOSOME I
5174	15040	24808	1.47	1.2E-01	Q10441	SWISSPROT	HYPOTHETICAL 52.4 KD PROTEIN C12B10.08C IN CHROMOSOME I
5199	15062		2.47	1.2E-01	AW401836.1	EST_HUMAN	UI-HF-BK0-aah-d-01-0-UI.1 NIH_MGC_36 Homo sapiens cDNA clone IMAGE:3053617 5'
5251	15174	24947	2.63	1.2E-01	W33035.1	EST_HUMAN	zc08d02.r1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:321699 5'
5297	15218	25021	1.9	1.2E-01	Z98286.1	NT	Homo sapiens gene encoding plakophilin (exons 1-13)
5762	15669	25776	1.69	1.2E-01	BE620945.1	EST_HUMAN	601493518F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3895613 5'
5806	15711	25824	2.19	1.2E-01	AW845275.1	EST_HUMAN	IL0-CT0031-221099-113-e04 CT0031 Homo sapiens cDNA
5839	15745	25858	1.56	1.2E-01	M26925.1	NT	Mouse galactosyltransferase mRNA, complete cds
6607	16487		1.21	1.2E-01	BE007072.1	EST_HUMAN	PM3-BN0137-290300-002-409 BN0137 Homo sapiens cDNA
6642	16522	26715	2.46	1.2E-01	A1913753.1	EST_HUMAN	wc99g03.x1 NCI_CGAP_C63 Homo sapiens cDNA clone IMAGE:2328804 3' similar to SW:GST2_HUMAN
6893	16772		9.72	1.2E-01	AW083652.1	EST_HUMAN	Q99795 MICROSOMAL GLUTATHIONE S-TRANSFERASE II ; xc49d07.x1 NCI_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:2587597 3' similar to gb:M13452 LAMIN A (HUMAN);
6904	16782		3.86	1.2E-01	AF053772.1	NT	Staphylococcus aureus plasmid pSK23 putative recombinase Sin (sin) gene, partial cds; and transcriptional regulator QacR (qacR) and multidrug efflux protein QacB (qacB) genes, complete cds
7043	16920		2.27	1.2E-01	U32714.1	NT	Haemophilus influenzae Rd section 29 of 163 of the complete genome
7521	17340	27546	1.5	1.2E-01	X77961.1	NT	S.cerevisiae HXT5 gene
7747	17597	27819	1.51	1.2E-01	AV710857.1	EST_HUMAN	AV710857 Cu Homo sapiens cDNA clone CUAAKE08 5'
8260	18140		2.95	1.2E-01	D26184.1	NT	Yeast MIP15 gene for suppressor protein, complete cds
8417	18291		3.35	1.2E-01	BE962324.2	EST_HUMAN	601655578R1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3846283 3'
8487	18360		1.93	1.2E-01	BF314481.1	EST_HUMAN	601900763F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4130103 5'
8579	18447	28715	2.6	1.2E-01	AF190493.1	NT	Homo sapiens dynein intermediate chain DNAI1 (DNAI1) gene, exon 17

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Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8798	18612		2.02	1.2E-01	M65109.1	NT	Rabbit glycogen-associated protein phosphatase regulatory subunit (RG1) mRNA, complete cds
9032	18822		2.22	1.2E-01	AV658033.1	EST_HUMAN	AV658033 GLC Homo sapiens cDNA clone GLCFB12 3'
9383	19043		2.78	1.2E-01	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
9458	19693	24897	2.58	1.2E-01	Q04912	SWISSPROT	MACROPHAGE-STIMULATING PROTEIN RECEPTOR PRECURSOR (MSP RECEPTOR) (P185-RON) (GDW136) (CD136 ANTIGEN)
9567	10476		7.69	1.2E-01	AF039442.1	NT	Homo sapiens colon cancer antigen NY-CO-45 mRNA, partial cds
9671	19230		1.41	1.2E-01	X53981.1	NT	R. norvegicus NF68 gene for 68kDa neurofilament
9739	19706	24903	2.36	1.2E-01	BE061418.1	EST_HUMAN	QV4-BT0234-111199-031-g10 BT0234 Homo sapiens cDNA
9761	19281	25231	3.68	1.2E-01	AI299903.1	EST_HUMAN	qn20g05.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1898840 3'
9782	19295		2.07	1.2E-01	L10187.1	NT	Xenopus laevis integrin alpha 3 subunit mRNA, partial cds
9786	19636		4.72	1.2E-01	O98433	SWISSPROT	CYCLIN T
9960	19424		2.18	1.2E-01	BF314481.1	EST_HUMAN	601900763F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4130103 5'
552	10493	20301	0.95	1.1E-01	AI561003.1	EST_HUMAN	Int18d08.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2167983 3'
599	10535	20344	3.38	1.1E-01	AA669006.1	EST_HUMAN	nm08g11.s1 NCI_CGAP_Cot10 Homo sapiens cDNA clone IMAGE:1058620 3' similar to gb:X06985_mai
1038	10956	20769	1.53	1.1E-01	BF697308.1	EST_HUMAN	HEME OXYGENASE 1 (HUMAN);
1069	10985		1.29	1.1E-01	AL161560.2	NT	602129847F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4286771 5'
1143	12686	20899	4.06	1.1E-01	AW972158.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 60
1229	11137	20990	1.72	1.1E-01	D64004.1	NT	EST384142 IMAGE resequences, MAGL Homo sapiens cDNA
1504	11408	21267	2.47	1.1E-01	AU140363.1	EST_HUMAN	Synechocystis sp. PCC6803 complete genome, 23/27, 2868767-3002965
2266	12150		2.25	1.1E-01	6756215	NT	AU140363 PLACE2 Homo sapiens cDNA clone PLACE2000403 5'
2492	12653		1.17	1.1E-01	6978676	NT	Mus musculus pre T-cell antigen receptor alpha (Pctra), mRNA
2520	12394		1.17	1.1E-01	AW821909.1	EST_HUMAN	Rattus norvegicus Procollagen II alpha 1 (Col2a1), mRNA
2825	12754	22546	1.84	1.1E-01	S82418.1	NT	RCO-ST0379-210100-032-g04 ST0379 Homo sapiens cDNA
2997	12925	22717	0.8	1.1E-01	F03295.1	EST_HUMAN	Interleukin-12 p35 subunit [mouse, Genomic, 700 nt, segment 4 of 5]
3299	13221		1.39	1.1E-01	6753231	NT	HSC1RF022 normalized infant brain cDNA Homo sapiens cDNA clone c-1rf02 3'
3374	13293	23062	3	1.1E-01	BE393186.1	EST_HUMAN	Mus musculus calcium channel, voltage-dependent, I type, alpha 1G subunit (Caena1g), mRNA
3405	13322	23123	1.54	1.1E-01	X62135.1	NT	601308679F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3627066 5'
3534	13450	23246	0.94	1.1E-01	Y07695.1	NT	C.reinhardtii nuclear gene on linkage group XIX
3648	13562	23348	1.23	1.1E-01	X52708.1	NT	A. limnerius gene for transposase
4021	13925	23698	1.31	1.1E-01	AW819412.1	EST_HUMAN	G.gallus gene encoding non-histone chromosomal protein HMG-14b, exons 4 and 5
4021	13925	23669	1.31	1.1E-01	AW819412.1	EST_HUMAN	MR3-ST0290-290100-025-g07 ST0290 Homo sapiens cDNA
4021	13925	23669	1.31	1.1E-01	AW819412.1	EST_HUMAN	MR3-ST0290-290100-025-g07 ST0290 Homo sapiens cDNA

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4027	13930		0.87	1.1E-01	AF030001.1	NT	Mus musculus major histocompatibility locus class III region: butyrophilin-like protein gene, partial cds; Notch4, PBX2, RAGE, lysophosphatidic acid acyl transferase-alpha, palmitoyl-protein thioesterase 2 (PPT2), CREB-RP, and tenascin X (TNX) genes, complete cds
4159	14059		7.93	1.1E-01	AF157066.1	NT	Drosophila melanogaster klarsicht protein (klar) mRNA, complete cds
4189	14089	23867	0.8	1.1E-01	AW802056.1	EST_HUMAN	IL5-UM0070-020500-068-a08 UM0070 Homo sapiens cDNA
4466	14360	24150	0.91	1.1E-01	AF064564.2	NT	Fugu rubripes neurofibromatosis type 1 (NF1), A-kinase anchor protein (AKAP84), BAW protein (BAW), and WSB1 protein (WSB1) genes, complete cds
4539	14432	24214	2.02	1.1E-01	S44957.1	NT	Tapa-1=Integral membrane protein TAPA-1 [mice, B cell lymphoma line 38C13, Genomic, 1973 nt, segment 1 of 7]
4725	14611	24397	1.26	1.1E-01	Y07695.1	NT	A. Immersus gene for transposase
4819	14702	24487	1.25	1.1E-01	D90908.1	NT	Synechocystis sp. PCC6803 complete genome, 10/27, 118886-1311234
5479	15399		1.43	1.1E-01	AA747216.1	EST_HUMAN	nx76a03.s1 NCL_CGAP_Ew1 Homo sapiens cDNA clone IMAGE:1268140 similar to contains Alu repetitive element/contains element MER35 repetitive element;
5562	15478	25551	1.54	1.1E-01	X68851.1	NT	S.pombe ste8 gene encoding protein kinase
5579	15494	25570	4.73	1.1E-01	M85533.1	NT	Providencia rettgeri penicillin G amidase gene
5672	15581	25681	1.46	1.1E-01	AJ007973.1	NT	Homo sapiens LGMD2B gene
5687	15596	25697	1.79	1.1E-01	BE769152.1	EST_HUMAN	PM3-FT0024-130600-004-f12 FT0024 Homo sapiens cDNA
5697	15606	25708	7.01	1.1E-01	AW853699.1	EST_HUMAN	RC3-CT0254-280999-011-a01 CT0254 Homo sapiens cDNA
5876	15782	25903	1.39	1.1E-01	AF035746.1	EST_HUMAN	AF035746 Human salivary gland cell line HSG Homo sapiens cDNA clone RL43
5985	15890	26012	3.48	1.1E-01	O69535	SWISSPROT	ACETYL-COENZYME A SYNTHETASE (ACETATE-COA LIGASE) (ACYL-ACTIVATING ENZYME)
6027	15931		2.9	1.1E-01	AF032922.1	NT	Homo sapiens syntxin 4 binding protein UNC-18c (UNC-18c) mRNA, complete cds
6068	16052	26198	2.21	1.1E-01	11432372	NT	Homo sapiens phosphatidylinositol glycan, class B (PIGB), mRNA
6448	16309	26474	7.05	1.1E-01	BF684628.1	EST_HUMAN	602140976F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4302019 5'
6448	16309	26475	7.05	1.1E-01	BF684628.1	EST_HUMAN	602140976F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4302019 5'
6513	16372	26550	1.74	1.1E-01	P41067	SWISSPROT	TRAB PROTEIN
6531	16390	26570	3.07	1.1E-01	AA788784.1	EST_HUMAN	af31b06.s1 Soares_parathyroid_tumor_NbH-PA Homo sapiens cDNA clone 1240403 3' similar to gb:J03483
6777	16659	26845	1.57	1.1E-01	AA493574.1	EST_HUMAN	CHROMOGRANIN A PRECURSOR (HUMAN);
6777	16656	26846	1.57	1.1E-01	AA493574.1	EST_HUMAN	rh04g10.s1 NCL_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943362
6803	16682	26872	1.22	1.1E-01	X91233.1	NT	rh04g10.s1 NCL_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943362
6826	16705		1.24	1.1E-01	AW817918.1	EST_HUMAN	H.sapiens IL15 gene
6862	16741	26934	1.78	1.1E-01	AL134349.1	EST_HUMAN	PM1-ST0270-080200-001-f09 ST0270 Homo sapiens cDNA
7118	16995	27186	2.19	1.1E-01	U02482.1	NT	DKFZp547P194_r1 547 (synonym: hfrb1) Homo sapiens cDNA clone DKFZp547P194 5'
							Pedococcus acidilactici H plasmid pSMB74 pediocin ACh production (pap) gene cluster papA, papB, papC and papD genes, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7228	17105	27294	2.24	1.1E-01	AA192153.1	EST_HUMAN	z983b12.r1 Striatogene muscle 937209 Homo sapiens cDNA clone IMAGE:627743 5'
7228	17105	27295	2.24	1.1E-01	AA192153.1	EST_HUMAN	z983b12.r1 Striatogene muscle 937209 Homo sapiens cDNA clone IMAGE:627743 5'
7287	17163	27362	2.48	1.1E-01	T72875.1	EST_HUMAN	y419h03.s1 Soares fetal liver spleen 1N1LS Homo sapiens cDNA clone IMAGE:108725 3' similar to gb:M81181 SODIUM/POTASSIUM-TRANSPORTING ATPASE BETA-2 (HUMAN);
7467	17327		2.08	1.1E-01	BF085149.1	EST_HUMAN	MR2-GN0027-040900-005-a08 GN0027 Homo sapiens cDNA
7861	17711		1.23	1.1E-01	R80590.1	EST_HUMAN	y96a09.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:147064 3'
8181	12925	22717	1.94	1.1E-01	F03265.1	EST_HUMAN	HSCIRF022 normalized infant brain cDNA Homo sapiens cDNA clone c-1f02 3'
8294	18173		3.88	1.1E-01	AF169032.1	NT	Carassius auratus activin beta A precursor, mRNA, complete cds
8402	18278	28530	2.93	1.1E-01	R23708.1	EST_HUMAN	yh35f12.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:131759 5' similar to contains Alu repetitive element; contains TAR1 repetitive element;
8519	18391	28655	1.95	1.1E-01	X70058.1	NT	M.musculus cytokine gene
8539	18411	28676	3.21	1.1E-01	Z11910.1	NT	Z.mobilis tgt and lig genes encoding tRNA guanine transglycosylase and DNA ligase
8539	18411	28677	3.21	1.1E-01	Z11910.1	NT	Z.mobilis tgt and lig genes encoding tRNA guanine transglycosylase and DNA ligase
8626	18491	28763	2.79	1.1E-01	P17437	SWISSPROT	SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN)
9241	18956		3.19	1.1E-01	BE767023.1	EST_HUMAN	RC2-NT0112-120600-014-03 NT0112 Homo sapiens cDNA
9485	19507		2.06	1.1E-01	BE974556.1	EST_HUMAN	601680551R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3850604 3'
9893	19372	25192	2.14	1.1E-01	BF239753.1	EST_HUMAN	601906350F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4134085 5'
1183	11094		4.08	1.0E-01	O62855	SWISSPROT	DEOXYRIBONUCLEASE II PRECURSOR (DNASE II) (ACID DNASE) (LYSOSOMAL DNASE II)
1251	11158	21007	1.89	1.0E-01	A1985499.1	EST_HUMAN	ws08d01.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2496577 3' similar to contains MER7.13 MER7 repetitive element;
1370	11276	21132	2.88	1.0E-01	AL161504.2	NT	Arabidopsis thaliana DNA chromosome 4, config fragment No. 16
2439	12316	22213	1	1.0E-01	AW451365.1	EST_HUMAN	UI-H-B13-alc-d-07-0-UJ.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2736420 3'
3468	13384	23189	0.98	1.0E-01	BF033991.1	EST_HUMAN	601458301F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3859849 5'
3658	13572	23359	1.01	1.0E-01	BF239818.1	EST_HUMAN	601906489F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4134071 5'
3871	13782	23574	2.44	1.0E-01	BF365703.1	EST_HUMAN	QV2-NT0048-160800-316-e05 NT0048 Homo sapiens cDNA
4307	14204	23987	1.5	1.0E-01	AE002265.2	NT	Chlamydomonas reinhardtii AR39, section 91 of 94 of the complete genome
4455	14349		1.17	1.0E-01	A1792349.1	EST_HUMAN	ar32c04.y5 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1700358 5'
4673	14501	24289	1.26	1.0E-01	U50450.1	NT	Drosophila melanogaster tyrosine kinase p45 isoform (fer) mRNA, complete cds
4838	14719	24502	2.06	1.0E-01	AW952344.1	EST_HUMAN	EST1364414 IMAGE resequences, MAGB Homo sapiens cDNA
5158	15025	24792	0.87	1.0E-01	D49683.1	NT	Mouse FIZ-F1 gene
5188	15051	24815	1.44	1.0E-01	BF15935.1	EST_HUMAN	UI-H-BW1-aca-e-12-0-UJ.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3084023 3'
5260	15182		9.16	1.0E-01	W86490.1	EST_HUMAN	zh62h04.s1 Soares fetal_liver_spleen_1N1LS_S1 Homo sapiens cDNA clone IMAGE:416695 3'
5670	15580	25680	11.21	1.0E-01	AF274875.1	NT	Homo sapiens growth factor receptor-bound protein 7 (GRB7) gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6187	16072		1.88	1.0E-01	R23821.1	EST_HUMAN	Yh34h06.r1 Scores placenta Nb2-IP Homo sapiens cDNA clone IMAGE:131675 5' similar to contains Alu repetitive element;
6549	16407		2.45	1.0E-01	Y12488.1	NT	M.musculus with gene
7299	17175	27376	1.16	1.0E-01	AF102855.2	NT	Rattus norvegicus synaptic SAPAP-interacting protein Synemon mRNA, complete cds
7473	17333		1.8	1.0E-01	M76729.1	NT	Human pro-alpha-1 (V) collagen mRNA, complete cds
7505	17293		2.73	1.0E-01	AE001501.1	NT	Helicobacter pylori, strain J99 section 62 of 132 of the complete genome
7651	17501	27724	1.84	1.0E-01	BF240164.1	EST_HUMAN	601905661F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4133487 5'
7713	17563	27788	9.08	1.0E-01	AB046799.1	NT	Homo sapiens mRNA for KIAA1579 protein, partial cds
7713	17563	27789	9.08	1.0E-01	AB046799.1	NT	Homo sapiens mRNA for KIAA1579 protein, partial cds
7918	17768	28007	1.26	1.0E-01	BE792750.1	EST_HUMAN	601584604F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3939096 5'
8050	17941		2.02	1.0E-01	AU159127.1	EST_HUMAN	AU159127 THYRO1 Homo sapiens cDNA clone THYRO1000895 3'
8393	18269	28520	2.9	1.0E-01	BF242946.1	EST_HUMAN	601877703F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4106089 5'
8393	18269	28521	2.9	1.0E-01	BF242946.1	EST_HUMAN	601877703F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4106089 5'
8703	18521	28803	4.43	1.0E-01	BE790543.1	EST_HUMAN	601582558F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3936734 5'
9226	19285		2.5	1.0E-01	BE637719.1	EST_HUMAN	601065554F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3451933 5'
9453	19085		1.34	1.0E-01	7662165	NT	Homo sapiens KIAA0514 gene product (KIAA0514), mRNA
9469	19098		2.03	1.0E-01	X00854.1	NT	Drosophila melanogaster ftz gene
9735	19688		2.57	1.0E-01	U52691.1	NT	Gonyaulax polyedra putative type-1 serine/threonine phosphatase (PP1) mRNA, complete cds
9765	19285		2.46	1.0E-01	BE537719.1	EST_HUMAN	601065554F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3451933 5'
9818	19664		8.59	1.0E-01	U68634.1	NT	Saccharomyces cerevisiae suppressor of ABF1 (SAB2) gene, complete cds
9871	19360	25187	1.28	1.0E-01	AJ271049.1	NT	Zea mays mRNA for Toc34-2 protein (toc34B gene)
9877	19363		4.16	1.0E-01	AP001507.1	NT	Bacillus halodurans genomic DNA, section 1/14
							Drosophila melanogaster cAMP-dependent protein kinase type II regulatory subunit (pka-R1I) mRNA, complete cds
2752	12614	22505	1.09	9.9E-02	AF274008.1	NT	
2757	12619	22511	1.44	9.9E-02	BE545554.1	EST_HUMAN	601070219F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3456365 5'
2757	12619	22512	1.44	9.9E-02	BE545554.1	EST_HUMAN	601070219F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3456365 5'
2950	12877	22675	0.92	9.9E-02	AV730747.1	EST_HUMAN	AV730747 HTF Homo sapiens cDNA clone HTFBND05 5'
3229	13153	22952	1.15	9.9E-02	AF099810.1	NT	Homo sapiens neurxin III-alpha gene, partial cds
4582	14472	24280	22.55	9.9E-02	BE674249.1	EST_HUMAN	7477c12.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3278698 3'
6161	15118	24862	7.96	9.9E-02	D83710.1	NT	Aspergillus terreus BSD mRNA for biastidin S deaminase, complete cds
7332	17236	27440	1.5	9.9E-02	6755111	NT	Mus musculus phospholipid transfer protein (Pltp), mRNA
551	10492		1.58	9.8E-02	X56338.1	NT	O. sativa PAMY3C gene for alpha-amylase
1711	11612	21482	1.53	9.8E-02	4503224	NT	Homo sapiens cytochrome P450, subfamily 1F, polypeptide 1 (CYP2F1) mRNA
3106	13032	22827	3.28	9.8E-02	AF184274.1	NT	Daucus carota leucoanthocyanidin dioxygenase 2 (LDOX) mRNA, LDOX-2 allele, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4131	14031	23805	6.67	9.8E-02	AF257329.1	NT	Leptosphaeria maculans beta-tubulin mRNA, complete cds
4131	14031	23806	6.67	9.8E-02	AF257329.1	NT	Leptosphaeria maculans beta-tubulin mRNA, complete cds
8755	17904	28148	2.1	9.8E-02	BF037421.1	EST_HUMAN	601460793F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3864287 5'
1328	11235	21092	1.16	9.7E-02	AB005908.1	NT	Aloe arborescens mRNA for NADP-malic enzyme, complete cds
1567	11471		0.98	9.7E-02	4503710	NT	Homo sapiens fibroblast growth factor receptor 3 (achondroplasia, thanatophoric dwarfism) (FGFR3) mRNA
2214	12100	22004	2.37	9.7E-02	BE168660.1	EST_HUMAN	QV1-HT0516-070300-095-a04 HT0516 Homo sapiens cDNA
3901	13811		3.56	9.7E-02	Q99795	SWISSPROT	CELL SURFACE A33 ANTIGEN PRECURSOR (GLYCOPROTEIN A33)
5661	15572	25669	1.39	9.7E-02	AW954476.1	EST_HUMAN	EST366546 IMAGE resequences, MAGC Homo sapiens cDNA
6321	16184	26345	4.27	9.7E-02	Z99119.1	NT	Bacillus subtilis complete genome (section 16 of 21): from 2997771 to 3213410
6655	16535	26731	1.59	9.7E-02	N22798.1	EST_HUMAN	yw41c03.s1 Weizmann Olfactory Epithelium Homo sapiens cDNA clone IMAGE:254788 3'
6655	16535	26732	1.59	9.7E-02	N22798.1	EST_HUMAN	yw41c03.s1 Weizmann Olfactory Epithelium Homo sapiens cDNA clone IMAGE:254788 3'
7137	17014	27207	1.32	9.7E-02	AI953984.1	EST_HUMAN	wx78b06.x1 NCL_CGAP_Ov68 Homo sapiens cDNA clone IMAGE:2549747 3' similar to gb.X62851_ma1
8531	18403		1.97	9.7E-02	U59337.1	NT	PEPTIDYL-PROLYL CIS-TRANS ISOMERASE A (HUMAN);
1969	11862	21753	1.27	9.6E-02	AI080721.1	EST_HUMAN	Mus musculus ligatin (Lgtn) mRNA, partial cds
1969	11862	21754	1.27	9.6E-02	AI080721.1	EST_HUMAN	oz47d11.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1678485 3'
4248	14147	23921	6.02	9.6E-02	Z32686.2	NT	oz47d11.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1678485 3'
4932	14810	24579	0.94	9.6E-02	AW966230.1	EST_HUMAN	Proteus mirabilis fimbrial operon, strain HI4320
5093	14963	24738	0.8	9.6E-02	BE061729.1	EST_HUMAN	EST378303 IMAGE resequences, MAGI Homo sapiens cDNA
5713	15621		2.72	9.6E-02	BE910039.1	EST_HUMAN	RC5-BT0254-031099-011-a03 BT0254 Homo sapiens cDNA
7502	17371	27580	1.51	9.6E-02	AV687898.1	EST_HUMAN	601498088F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3900185 5'
7677	17527		1.84	9.6E-02	BE894895.1	EST_HUMAN	AV687898 GKO Homo sapiens cDNA clone GKCAAH02 5'
7772	17622	27855	1.75	9.6E-02	AJ243211.1	NT	601494080F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3919383 5'
7839	17689	27933	1.59	9.6E-02	AB013985.1	NT	Homo sapiens DMBT1 candidate tumour suppressor gene, exons 1 to 55
7839	17689	27934	1.59	9.6E-02	AB013985.1	NT	Homo sapiens DMBT1 candidate tumour suppressor gene, exons 1 to 55
7886	17736	27980	3.29	9.6E-02	P08174	SWISSPROT	Antirrhinum majus transposon Tam3 pseudogene for transposase (in S-5 copy)
8125	18013	28260	6.51	9.6E-02	Z79702.1	NT	Antirrhinum majus transposon Tam3 pseudogene for transposase (in S-5 copy)
8957	18764	29056	1.8	9.6E-02	AA825755.1	EST_HUMAN	COMPLEMENT DECAY-ACCELERATING FACTOR PRECURSOR (CD55)
9798	19312		1.38	9.6E-02	H14599.1	EST_HUMAN	Mycobacterium tuberculosis H37Rv complete genome, segment 102/162
9848	19344	25212	1.26	9.6E-02	BE728219.1	EST_HUMAN	zu91g01.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:745392 3'
4012	13918	23694	2.25	9.5E-02	AW992395.1	EST_HUMAN	ym19h03.s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:48653 3'
5062	14932	24704	0.87	9.5E-02	U63374.1	NT	601563355F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3832908 5'
							CM2-BN0023-050200-087-f12 BN0023 Homo sapiens cDNA
							Lycopodium esculentum polygalacturonase isoenzyme 1 beta subunit gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6323	16186	26348	3.72	9.5E-02	AB003473.1	NT	Trimerus flaviviridis DNA for phospholipase A2 inhibitor, complete cds
6467	16327	26494	7.46	9.5E-02	AL161538.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 38
6599	16479	26666	2.59	9.5E-02	BF035861.1	EST_HUMAN	601453642F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3857243 5'
6599	16479	26667	2.59	9.5E-02	BF035861.1	EST_HUMAN	601453642F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3857243 5'
8066	17957	28206	3.29	9.5E-02	BF035861.1	EST_HUMAN	601453642F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3857243 5'
8066	17957	28207	3.29	9.5E-02	BF035861.1	EST_HUMAN	601453642F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3857243 5'
1792	11690	21565	3.86	9.4E-02	BF671063.1	EST_HUMAN	602150882F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4291917 5'
1820	11717	21597	0.86	9.4E-02	U55944.1	NT	Cavia porcellus 3beta-hydroxysteroid sulfotransferase mRNA, complete cds
1820	11717	21598	0.86	9.4E-02	U55944.1	NT	Cavia porcellus 3beta-hydroxysteroid sulfotransferase mRNA, complete cds
3804	13716	23604	4.34	9.4E-02	Z33069.1	NT	M. capricolus DNA for CONTIG MC073
4980	14855	24621	0.89	9.4E-02	6753517	NT	Mus musculus coding region determinant-binding protein (Crdp), mRNA
6999	16876		2.62	9.4E-02	Z46863.1	NT	Acinetobacter sp. cysD, cobQ, cobQ, lysS, rubA, rubB, estB, oxyR, ppk, migA, ORF2 and ORF3 genes
8304	16338	26505	2.69	9.4E-02	L78833.1	NT	Human BRCA1, Rho7 and val genes, complete cds, and ipf35 gene, partial cds
9083	19603		3.36	9.4E-02	U31815.1	NT	Rattus norvegicus calcium channel alpha-1C subunit (ROB2) mRNA, partial cds
9943	19411	25182	1.42	9.4E-02	U27699.1	NT	Human pephBG1-1 betaine-GABA transporter mRNA, complete cds
2960	12887		1.83	9.3E-02	4809280	NT	Homo sapiens BAI1-associated protein 3 (BAIAP3) mRNA
2993	12921		5.39	9.3E-02	6912525	NT	Homo sapiens nasopharyngeal epithelium specific protein 1 (NESG1), mRNA
3218	13142	22946	2.03	9.3E-02	BF575511.1	EST_HUMAN	602133086F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4288289 5'
4060	13962	23738	3.51	9.3E-02	BE991943.1	EST_HUMAN	601266082F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607653 5'
4060	13962	23739	3.51	9.3E-02	BE991943.1	EST_HUMAN	601266082F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607653 5'
4628	14516		1.88	9.3E-02	AV732224.1	EST_HUMAN	AV732224 HTF Homo sapiens cDNA clone HTFAUA06 5'
7599	17450	27665	2.24	9.3E-02	BE962831.2	EST_HUMAN	601655988R1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3855981 3'
7855	17705	27949	3.52	9.3E-02	Q15034	SWISSPROT	HYPOTHETICAL PROTEIN KIAA0032
7855	17705	27950	3.52	9.3E-02	Q15034	SWISSPROT	HYPOTHETICAL PROTEIN KIAA0032
7913	17763		3.74	9.3E-02	AW206117.1	EST_HUMAN	U1-H-B1 afx-h-05-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2723553 3'
9343	19527		1.85	9.3E-02	AJ249850.1	NT	Photobacterium damsela subsp. damsela partial gyrB gene for DNA gyrase B subunit
9704	19555		8.62	9.3E-02	AW468850.1	EST_HUMAN	hd28h12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2910887 3'
9896	19602		1.95	9.3E-02	AF100956.1	NT	Mus musculus major histocompatibility locus class II region; Fas-binding protein Daxx (DAXX) gene, partial cds; Bing1 (BING1), tapasin (tapasin), RalGDS-like factor (RLF), KE2 (KE2), BING4 (BING4), beta1, 3-galactosyl transferase (beta1,3-galactosyl tr)
228	10197	20008	4.32	9.2E-02	U60315.1	NT	Molluscum contagiosum virus subtype 1, complete genome
228	10197	20009	4.32	9.2E-02	U60315.1	NT	Molluscum contagiosum virus subtype 1, complete genome
228	10197	20010	4.32	9.2E-02	U60315.1	NT	Molluscum contagiosum virus subtype 1, complete genome

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2180	12067		2.2	9.2E-02	R54156.1	EST_HUMAN	y98f07.r1 Soares infant brain (NIB Homo sapiens cDNA clone IMAGE:41618 5'
3142	13067	22866	4.53	9.2E-02	Q28631	SWISSPROT	MAJOR EPIDIDYMIS-SPECIFIC PROTEIN E4 (EPIDIDYMAL PROTEIN BE-20)
3265	13188	22986	1.16	9.2E-02	AA534354.1	EST_HUMAN	nt79e01.s1 NCI_CGAP_C03 Homo sapiens cDNA clone IMAGE:926136 3'
3537	13453		1.12	9.2E-02	6755215	NT	Mus musculus pre T-cell antigen receptor alpha (Pitera), mRNA
4145	14045		1.34	9.2E-02	U92048.1	NT	Human herpesvirus 1 strain KOS-63, latency-associated transcript, promoter region
4211	14109		1.02	9.2E-02	BE299722.1	EST_HUMAN	600944365F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2960176 5'
4538	14431	24213	1.86	9.2E-02	X96402.1	NT	G.gallus Mia-CK gene
6670	16550	26746	1.86	9.2E-02	T49920.1	EST_HUMAN	y989c09.r1 Stratagene placenta (#937225) Homo sapiens cDNA clone IMAGE:69808 5' similar to similar to gb:Y56009 GUANINE NUCLEOTIDE-BINDING PROTEIN G(S), ALPHA SUBUNIT (HUMAN)
6756	16635	26823	2.07	9.2E-02	X95256.1	NT	H.vulgaris xylose isomerase gene
417	9984	19776	2.77	9.1E-02	X77665.1	NT	O. cuniculus K12 keratin gene
2365	12245	22139	1.01	9.1E-02	P78985	SWISSPROT	6-PHOSPHOFRUCTOKINASE (PHOSPHOFRUCTOKINASE) (PHOSPHOHEXOKINASE)
3618	13532		1.14	9.1E-02	AW372569.1	EST_HUMAN	PM2-BT0349-161299-001-402 BT0349 Homo sapiens cDNA
4383	14279	24058	1.81	9.1E-02	AL161554.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 54
5507	15425	25487	1.73	9.1E-02	AF129756.1	NT	Homo sapiens MSH55 gene, partial cds; and CLIC1, DDAH, G6b, G6c, G6d, G6e, G6f, BAT5, G5b, CSK2B, BAT4, G4, Apo M, BAT3, BAT2, ALF-1, 1C7, LST-1, LTB, TNF, and LTA genes, complete cds
6372	16234	26393	11.89	9.1E-02	AW160658.1	EST_HUMAN	au74a05.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2781988 5'
7958	17808		1.65	9.1E-02	T02984.1	EST_HUMAN	FB19F10 Fetal brain, Stratagene Homo sapiens cDNA clone FB19F10 3' end
9021	18815		1.29	9.1E-02	9633494	NT	Bacteriophage Mu, complete genome
9256	19692		1.52	9.1E-02	AA179901.1	EST_HUMAN	zp38h12.s1 Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:611783 3' similar to SW:TRT3_HUMAN P45378 TROPONIN T, FAST SKELETAL MUSCLE, ISOFORM BETA ;
9785	19548		5.63	9.1E-02	AJ291390.1	NT	Homo sapiens partial MUC3B gene for MUC3B mucin, exons 1-11
727	10659	20490	3.36	9.0E-02	P15328	SWISSPROT	FOLATE RECEPTOR ALPHA PRECURSOR (FR-ALPHA) (FOLATE RECEPTOR 1) (FOLATE RECEPTOR, ADULT) (ADULT FOLATE-BINDING PROTEIN) (FBP) (OVARIAN TUMOR-ASSOCIATED ANTIGEN MOV18) (KB CELLS FBP)
1617	11521	21379	6.45	9.0E-02	BE220482.1	EST_HUMAN	h39g10.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3175942 3' similar to contains Alu repetitive element
2772	12634	22528	1.11	9.0E-02	AF138522.1	NT	HIV-1 p8c095-06 from USA envelope glycoprotein (env) gene, partial cds
2772	12634	22629	1.11	9.0E-02	AF138522.1	NT	HIV-1 p8c095-06 from USA envelope glycoprotein (env) gene, partial cds
3294	13216	23018	0.92	9.0E-02	AF279135.1	NT	Dicystellum discoidium spore coat structural protein SP65 (colE) gene, complete cds
4202	14101	23883	0.8	9.0E-02	S68757.1	NT	corticosteroid-binding globulin [Saimiri sciureus=squirrel monkeys, liver, mRNA, 1474 nt]
4202	14101	23884	0.8	9.0E-02	S68757.1	NT	corticosteroid-binding globulin [Saimiri sciureus=squirrel monkeys, liver, mRNA, 1474 nt]
4321	14218	24001	1.2	9.0E-02	P55286	SWISSPROT	LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ)

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4568	14460	24248	1.79	9.0E-02	X65740.2	NT	Plasmodium falciparum P-type ATPase 3 gene
5142	15009	24780	1.06	9.0E-02	Q24597	SWISSPROT	REGULATORY PROTEIN ZESTE
5647	15560	25653	8.02	9.0E-02	W56037.1	EST_HUMAN	za68a12.r1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:297694 5' similar to PIR:S52171 S52171 small G protein - human ;
9967	19428		15.35	9.0E-02	11431759	NT	Homo sapiens chromosome 16 open reading frame 5 (C16orf5), mRNA
1419	11325	21189	2.15	8.9E-02	BF701593.1	EST_HUMAN	602129030F2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285951 5'
1419	11325	21190	2.15	8.9E-02	BF701593.1	EST_HUMAN	602129030F2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285951 5'
2338	12218	22117	1.41	8.9E-02	BE153572.1	EST_HUMAN	PMO-HT0339-251199-003-d01 HT0339 Homo sapiens cDNA
4104	14004		1.71	8.9E-02	AF286055.1	NT	Atrichum angustatum AtranFlo2 protein (AtranFlo2) gene, partial cds
4534	14427	24208	0.92	8.9E-02	AA424887.1	EST_HUMAN	zw03d04.s1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:768199 3'
5569	15485	25559	3.3	8.9E-02	AW452122.1	EST_HUMAN	U-H-B13-alo-f08-0-J1.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:3068294 3'
5569	15485	25560	3.3	8.9E-02	AW452122.1	EST_HUMAN	U-H-B13-alo-f08-0-J1.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:3068294 3'
5576	15491	25568	3.13	8.9E-02	11433478	NT	Homo sapiens similar to endoglycan (H. sapiens) (LOC63107), mRNA
6270	16135	26290	1.56	8.9E-02	P47259	SWISSPROT	FOLD BIFUNCTIONAL PROTEIN [INCLUDES: METHYLENE TETRAHYDROFOLATE DEHYDROGENASE; METHENYL TETRAHYDROFOLATE CYCLOHYDROLASE]
6460	16320		1.83	8.9E-02	Z79021.1	NT	H. sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA20F8
6998	16875	27066	5.28	8.9E-02	AA309319.1	EST_HUMAN	EST180187 Liver, hepatocellular carcinoma Homo sapiens cDNA 5' end
9228	18949		4.03	8.9E-02	BF696918.1	EST_HUMAN	602129682F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4286180 5'
1351	11257	21113	1.25	8.8E-02	Q27474	SWISSPROT	PROBABLE DNA LIGASE (POLYDEOXYRIBONUCLEOTIDE SYNTHASE [ATP])
3828	13740	23532	0.96	8.8E-02	AA299128.1	EST_HUMAN	EST11595 Uterus Homo sapiens cDNA 5' end
3948	13856		3.24	8.8E-02	O00268	SWISSPROT	TRANSCRIPTION INITIATION FACTOR TH1D 135 KDA SUBUNIT (TAFII-135) (TAFII-130)
4205	14104		1.13	8.8E-02	4580423	NT	Homo sapiens paired box gene 6 (aniridia, keratitis) (PAX6), isoform b, mRNA
7195	17072	27260	1.83	8.8E-02	AA151872.1	EST_HUMAN	zne9a05.s1 Stratagene colon (#937204) Homo sapiens cDNA clone IMAGE:566288 3'
8461	18334	28596	3.19	8.8E-02	BE264455.1	EST_HUMAN	601191770F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3535648 5'
8461	18334	28597	3.19	8.8E-02	BE264455.1	EST_HUMAN	601191770F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3535648 5'
8585	18453	28722	10.63	8.8E-02	AL040129.1	EST_HUMAN	DKFZp434D1313_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434D1313 5'
9302	19001	25332	1.38	8.8E-02	Z71561.1	NT	S. cerevisiae chromosome XIV reading frame ORF_YNL285w
3636	13550	23337	3.02	8.7E-02	U82695.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
3636	13550	23338	3.02	8.7E-02	U82695.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3879	13790	23578	0.82	8.7E-02	W87841.1	EST_HUMAN	zh68a02.r1 Soares_fetal_liver_nFLS_S1 Homo sapiens cDNA clone IMAGE:417194 5' similar to contains element MER12 repetitive element;
4609	14497	24286	1.22	8.7E-02	AF178836.1	NT	Mus musculus JNK interacting protein-3a (Jip3) mRNA, complete cds
5034	14906		1.06	8.7E-02	AE000895.1	NT	Methanobacterium thermoautotrophicum from bases 1176181 to 1189406 (section 101 of 148) of the complete genome
5255	15177	24951	5.41	8.7E-02	AA286875.1	EST_HUMAN	zs55g08.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:701438 3'
5255	15177	24952	5.41	8.7E-02	AA286875.1	EST_HUMAN	zs55g08.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:701438 3'
8094	17985		2.58	8.7E-02	U04758.1	NT	Oryctolagus cuniculus cytochrome P-450 (CYP4A4) gene, 5' end
8631	18496	28770	1.77	8.7E-02	AJ007763.1	NT	Glucuronobacter oxydans tRNA-Ile and tRNA-Ala genes
9293	18994		2.58	8.7E-02	X17116.1	NT	Human DNA for immunoglobulin alpha heavy chain from a case of alpha heavy chain disease
9484	19105		1.81	8.7E-02	6679057	NT	Mus musculus nidogen 2 (Nid2), mRNA
1232	11139	20991	7.05	8.6E-02	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
2197	12084	21986	2.22	8.6E-02	BE408667.1	EST_HUMAN	601304016F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638643 5'
3151	13076	22878	2.94	8.6E-02	U05468.1	NT	Trichomonas vaginalis beta-tubulin (btub1) gene, complete cds
3593	13507		3.07	8.6E-02	AF153362.1	NT	Dicystidium discoidium adenyl cyclase (acrA) gene, complete cds
4385	14281	24060	0.87	8.6E-02	U68179.1	NT	Oryctolagus cuniculus galactin-3 gene, untranslated exon and 5' flanking region
5708	15616	25718	4.38	8.6E-02	Y10826.1	NT	Homo sapiens LCN1b gene
5846	15752	25867	1.51	8.6E-02	J00440.1	NT	Mouse germline IgM chain gene, D region; D-q52, mu switch region (part a)
5846	15752	25868	1.51	8.6E-02	J00440.1	NT	Mouse germline IgM chain gene, D region; D-q52, mu switch region (part a)
6628	16508	26895	1.26	8.6E-02	5730066	NT	Homo sapiens Smf2-related CBP activator protein (SRCAP) mRNA
6628	16508	26896	1.26	8.6E-02	5730066	NT	Homo sapiens Smf2-related CBP activator protein (SRCAP) mRNA
8315	18192	28441	1.98	8.6E-02	AF208651.1	NT	Lacerta media cytochrome c oxidase subunit 1 gene, partial cds; mitochondrial gene for mitochondrial product
8315	18192	28442	1.98	8.6E-02	AF208651.1	NT	Lacerta media cytochrome c oxidase subunit 1 gene, partial cds; mitochondrial gene for mitochondrial product
8574	18442	28710	3.63	8.6E-02	BF305606.1	EST_HUMAN	601893437F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4139216 5'
8574	18442	28711	3.63	8.6E-02	BF305606.1	EST_HUMAN	601893437F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4139216 5'
8738	17887	28131	4.71	8.6E-02	AE001073.1	NT	Archaeoglobus fulgidus section 34 of 172 of the complete genome
8858	18670	28958	1.73	8.6E-02	AF283660.1	NT	Bacillus stearothermophilus BstFI methylase (FIM) and BstFI restriction endonuclease (FIR) genes, complete cds
2347	12227	22124	2.87	8.5E-02	AE000652.1	NT	Helicobacter pylori 26695 section 130 of 134 of the complete genome
5500	15419		1.8	8.5E-02	P08089	SWISSPROT	M PROTEIN, SEROTYPE 6 PRECURSOR
5658	15570	25665	5.34	8.5E-02	AF233885.1	NT	Mus musculus phospholipase C-like protein mRNA, partial cds
7003	16880	27072	1.93	8.5E-02	6754779	NT	Mus musculus myosin XV (Myo15), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7661	17511	27737	3.07	8.5E-02	BE833054.1	EST_HUMAN	RC4-OT0037-200700-014-e05 OT0037 Homo sapiens cDNA
7661	17511	27738	3.07	8.5E-02	BE833054.1	EST_HUMAN	RC4-OT0037-200700-014-e05 OT0037 Homo sapiens cDNA
8496	18369		11.15	8.5E-02	AF155510.1	NT	Homo sapiens heparanase precursor, mRNA, complete cds
8512	18384	28649	4.07	8.5E-02	AB001562.1	NT	Streptococcus mutans gene for glucose-1-phosphate uridylyltransferase, complete cds
9681	19488		1.39	8.5E-02	AJ005586.1	NT	Antirrhinum majus mRNA for MYB-related transcription factor
9841	19339		3.28	8.5E-02	AA362934.1	EST_HUMAN	EST72736 Ovary II Homo sapiens cDNA 5' end
2632	12728	22391	4.24	8.4E-02	W69330.1	EST_HUMAN	zd44e11.1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:343532 5'
5253	15175	24949	7.82	8.4E-02	BE267153.1	EST_HUMAN	601190436F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3534393 5'
6019	15923	26053	1.71	8.4E-02	AK024458.1	NT	Homo sapiens mRNA for FLJ00050 protein, partial cds
6680	16560	26755	8.11	8.4E-02	BE095074.1	EST_HUMAN	CM3-BT0750-260400-162-d05 BT0790 Homo sapiens cDNA
7931	17781	28020	1.44	8.4E-02	AI735184.1	EST_HUMAN	as88g10.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2335842 3' similar to TR:O88312
1965	11859	21748	0.86	8.3E-02	5835680	NT	Ixodes hexagonus mitochondrion, complete genome
1965	11869	21749	0.86	8.3E-02	5835680	NT	Ixodes hexagonus mitochondrion, complete genome
3544	13460	23254	6.19	8.3E-02	P75334	SWISSPROT	HYPOTHETICAL LIPOPROTEIN MG309 HOMOLOG PRECURSOR
3567	13481	23271	0.88	8.3E-02	AI436797.1	EST_HUMAN	th82g06.x1 Soares_NhhMPu_S1 Homo sapiens cDNA clone IMAGE:2125210 3'
3567	13481	23272	0.88	8.3E-02	AI436797.1	EST_HUMAN	th82g06.x1 Soares_NhhMPu_S1 Homo sapiens cDNA clone IMAGE:2125210 3'
5840	15746	25859	2.82	8.3E-02	AF052683.1	NT	Homo sapiens protocadherin 43 gene, exon 1
6653	16533	26728	3.42	8.3E-02	AF195787.1	NT	Rattus norvegicus dystrophin-related protein 2 A-form splice variant (Drp2) mRNA, complete cds
6671	16551		1.47	8.3E-02	AA865285.1	EST_HUMAN	cg88g08.s1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1455422 3' similar to contains L1.t1 L1 L1
6829	16708		1.42	8.3E-02	AA987873.1	EST_HUMAN	repetitive element;
7498	17368	27573	1.44	8.3E-02	AW583503.1	EST_HUMAN	cg81f10.s1 NCI_CGAP_Kid6 Homo sapiens cDNA clone IMAGE:1592779 3'
7506	17294		1.94	8.3E-02	AL161595.2	NT	la05h10.x1 Human Pancreatic Islets Homo sapiens cDNA 3' similar to TR:Q15332 Q15332 GAMMA
9307	16695		1.55	8.3E-02	BE968458.1	EST_HUMAN	SUBUNIT OF SODIUM POTASSIUM ATPASE LIKE. ;
1357	11263		7.82	8.2E-02	Y08170.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 91
1480	11385	21248	1.21	8.2E-02	AF167077.2	NT	601644770F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3929993 5'
3036	12964		1.78	8.2E-02	AL163206.2	NT	Gallus gallus mRNA for OBCAM protein gamma isoform
3733	13645		1.26	8.2E-02	AL161498.2	NT	Canis familiaris glutamate transporter (EAAT4) mRNA, complete cds
3926	13835	23615	1.11	8.2E-02	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C006
4187	14087	23862	5.36	8.2E-02	P48960	SWISSPROT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 10
4187	14087	23863	5.36	8.2E-02	P48960	SWISSPROT	Homo sapiens chromosome 21 segment HS21C006
4187	14087	23864	5.36	8.2E-02	P48960	SWISSPROT	LEUCOCYTE ANTIGEN CD97 PRECURSOR
4187	14087	23864	5.36	8.2E-02	P48960	SWISSPROT	LEUCOCYTE ANTIGEN CD97 PRECURSOR

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Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5014	14888	24655	2.82	8.2E-02	U76009.1	NT	Mus musculus zinc transporter (ZnT-3) gene, complete cds
5271	15193	24988	1.43	8.2E-02	BE897030.1	EST_HUMAN	601439576F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924523 5'
6188	16073	26222	3.14	8.2E-02	AF309555.1	NT	Bos taurus connective tissue growth factor precursor (CTGF) gene, complete cds
7094	16971	27164	3.13	8.2E-02	AW875126.1	EST_HUMAN	RC2-PT0004-031299-011-305 PT0004 Homo sapiens cDNA
7536	17387	27598	5.33	8.2E-02	X04197.1	NT	Beet necrotic yellow vein virus RNA-2
7628	17479	27699	2.11	8.2E-02	BE254318.1	EST_HUMAN	601115055F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3355508 5'
9314	19006	25336	4.13	8.2E-02	AE002246.2	NT	Chlamydomonas reinhardtii AR39, section 73 of 94 of the complete genome
9706	19480		1.84	8.2E-02	AF275366.1	NT	Mus musculus epidermal growth factor receptor (Egfr) gene, exons 5 through 28, and complete cds, alternatively spliced
1479	11384	21247	1.72	8.1E-02	AB017138.1	NT	Pseudomonas putida malonate decarboxylase gene cluster (mdcA, mdcB, mdcC, mdcD, mdcE, mdcG, mdcH, mdcL and mdcM genes), complete cds
7703	17553		1.65	8.1E-02	AY005150.1	NT	Homo sapiens extracellular glycoprotein lacritin precursor, gene, complete cds
8789	18604	28894	3.38	8.1E-02	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
5	12657	19784	3.28	8.0E-02	AW954653.1	EST_HUMAN	EST366723 MAGE resequences, MAGE Homo sapiens cDNA
920	10844	20860	1.33	8.0E-02	U60315.1	NT	Molluscum contagiosum virus subtype 1, complete genome
1671	12701	21440	10.54	8.0E-02	D26535.1	NT	Human gene for dihydrodipicolinate succinyltransferase, complete cds (exon 1-15)
1671	12701	21441	10.54	8.0E-02	D26535.1	NT	Human gene for dihydrodipicolinate succinyltransferase, complete cds (exon 1-15)
1861	11757	21632	3.9	8.0E-02	BE067219.1	EST_HUMAN	PM3-BT0347-170200-001-b08 BT0347 Homo sapiens cDNA
2323	12204	22103	1.01	8.0E-02	D90915.1	NT	Synechocystis sp. PCC6803 complete genome, 17/27, 2137259-2267259
2323	12204	22104	1.01	8.0E-02	D90915.1	NT	Synechocystis sp. PCC6803 complete genome, 17/27, 2137259-2267259
2421	12298		4.08	8.0E-02	BF246744.1	EST_HUMAN	601855548F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4075619 5'
2790	10991	20833	0.81	8.0E-02	M23449.1	NT	Dictyosellum discoideum cyclic nucleotide phosphodiesterase gene, complete cds
2870	12797	22591	1.01	8.0E-02	AL445067.1	NT	Thermoplasma acidophilum complete genome; segment 5/5
3745	13658	23440	0.84	8.0E-02	AW968118.1	EST_HUMAN	EST378191 MAGE resequences, MAGE Homo sapiens cDNA
3980	13887		1.06	8.0E-02	4503034	NT	Homo sapiens cAMP responsive element binding protein-like 2 (CREBL2) mRNA
4709	14595		5.62	8.0E-02	X72794.1	NT	M.musculus gene for gelatinase B
4834	14716	24499	0.87	8.0E-02	M28071.1	NT	Herpesvirus saimiri transformation-associated protein (STP), and dihydrofolate reductase (DHFR) gene, s complete cds, and small nuclear RNAs (uRNAs)
5591	15506	25581	3.35	8.0E-02	AF275948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
6261	15506	25581	1.63	8.0E-02	AF275948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
6727	16607	26798	3.65	8.0E-02	AL114993.1	NT	Boltylis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
7401	17268	27471	1.49	8.0E-02	X74208.1	NT	H.sapiens AGT gene, intron 4
7401	17268	27472	1.49	8.0E-02	X74208.1	NT	H.sapiens AGT gene, intron 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8172	18060	28310	7.42	8.0E-02	AF217796.1	NT	Homo sapiens SCG10 like-protein, helicase-like protein NHL, M68, and ADP-ribosylation factor related protein 1 (ARFRP1) genes, complete cds
9344	19023	25300	2.94	8.0E-02	AJ005375.1	NT	Drosophila oreana hunchback region
9881	13887		1.47	8.0E-02	4503034	NT	Homo sapiens cAMP responsive element binding protein-like 2 (CREBL2) mRNA
9989	19684		3.04	8.0E-02	AJ278435.1	NT	Mus musculus Ranbp7 gene, Stat gene and Wee1 gene
2127	12015	21913	3.98	7.9E-02	BE250008.1	EST_HUMAN	600943191F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2859810 5'
							ar88c08.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2173646 3' similar to gb:Z26876
2948	12875	22673	6.43	7.9E-02	AI582029.1	EST_HUMAN	60S RIBOSOMAL PROTEIN L38 (HUMAN);
3776	13688	23471	3.31	7.9E-02	6681044	NT	Mus musculus colony stimulating factor 1 receptor (Csf1r), mRNA
3776	13688	23472	3.31	7.9E-02	6681044	NT	Mus musculus colony stimulating factor 1 receptor (Csf1r), mRNA
4595	14483	24269	1.06	7.9E-02	BF348454.1	EST_HUMAN	602019770F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4155401 5'
4706	14592		1.16	7.9E-02	AB008019.1	NT	Arabidopsis thaliana RXW24L mRNA, partial cds
6882	16562	26756	3.25	7.9E-02	U27832.1	NT	Saccharomyces cerevisiae suppressor of MIF2 Smt4p (SMT4) gene, complete cds
7762	17612	27838	5.68	7.9E-02	AI081644.1	EST_HUMAN	ou63b05.s1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1632465 3' similar to WP:C37A2.2
7762	17612	27839	5.68	7.9E-02	AI081644.1	EST_HUMAN	ou63b05.s1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1632465 3' similar to WP:C37A2.2
1192	11102	20947	1.43	7.8E-02	AI793275.1	EST_HUMAN	ou63b05.s1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1570467 5' similar to contains L1.13 L1
1192	11102	20948	1.43	7.8E-02	AI793275.1	EST_HUMAN	ou63b05.s1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1570467 5' similar to contains L1.13 L1
4688	14574	24371	0.81	7.8E-02	BE836331.1	EST_HUMAN	PM3-FN0058-140700-005-f09 FN0058 Homo sapiens cDNA
5019	13603		2.71	7.8E-02	BE250048.1	EST_HUMAN	600943055F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2859863 5'
5197	15060	24825	1.04	7.8E-02	AI418620.1	EST_HUMAN	tg48g12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2112070 3' similar to contains MER10.13 MER10 repetitive element;
7236	17113	27306	2.06	7.8E-02	AF233437.1	NT	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP1b mRNA, complete cds
7236	17113	27307	2.06	7.8E-02	AF233437.1	NT	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP1b mRNA, complete cds
7389	17307	27513	1.27	7.8E-02	AA469354.1	EST_HUMAN	nc88b06.r1 NCI_CGAP_Prl1 Homo sapiens cDNA clone IMAGE:771731
1378	12693	21139	1	7.7E-02	AF181897.1	NT	Homo sapiens WRN (WRN) gene, complete cds
3538	13454		2.09	7.7E-02	AJ238093.1	NT	Homo sapiens partial AF-4 gene, exons 2 to 7 and Alu repeat elements
6615	16495	26682	4.4	7.7E-02	AA402949.1	EST_HUMAN	zu53d11.r1 Soares ovary tumor NBHOT Homo sapiens cDNA clone IMAGE:741717 5' similar to TR:G1173905 G1173905 SPLICEOSOME ASSOCIATED PROTEIN.;

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7660	17510	27736	4.62	7.7E-02	P38080	SWISSPROT	PROBABLE SERINE/THREONINE-PROTEIN KINASE YBR059C
8376	18253	28504	5.24	7.7E-02	11422757	NT	Homo sapiens KIAA0628 gene product (KIAA0628), mRNA
9535	19561		2	7.7E-02	11438859	NT	Homo sapiens Interferon regulatory factor 7 (IRF7), mRNA
3341	13261	23067	2.57	7.6E-02	BE514432.1	EST_HUMAN	601316426F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3634903 5'
3362	13281	23081	0.94	7.6E-02	AA298447.1	EST_HUMAN	EST112214 Cerebellum II Homo sapiens cDNA 5' and similar to protocadherin 43
3512	13428	23229	0.93	7.6E-02	AJ400877.1	NT	Homo sapiens ASCL3 gene, CEGP1 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene
4765	14650		0.96	7.6E-02	AW858844.1	EST_HUMAN	RC3-CT0347-110300-014-a05 CT0347 Homo sapiens cDNA
7383	17311	27518	1.34	7.6E-02	AJ131016.1	NT	Homo sapiens SCL gene locus
7685	17545		1.34	7.6E-02	AL139078.2	NT	Campylobacter jejuni NCITC11168 complete genome; segment 5/6
8927	18735	29028	2.45	7.6E-02	AW996645.1	EST_HUMAN	QV3-BN0046-150400-151-e04 BN0046 Homo sapiens cDNA
767	10698	20535	1.13	7.5E-02	5902093	NT	Homo sapiens solute carrier family 6 (neurotransmitter transporter, glycine), member 9 (SLC6A9), mRNA
767	10698	20536	1.13	7.5E-02	5902093	NT	Homo sapiens solute carrier family 6 (neurotransmitter transporter, glycine), member 9 (SLC6A9), mRNA
1878	11774	21649	0.87	7.5E-02	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
4407	14301	24085	0.84	7.5E-02	AB015961.1	NT	Homo sapiens IL-18 gene for interleukin-18, intron 1 and exon 2
6855	16734	26927	1.19	7.5E-02	AJ884367.1	EST_HUMAN	wf52b02.x1 NCL CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2428491 3' similar to gb:M14328 ALPHA ENOLASE (HUMAN);
6953	16831	27024	1.21	7.5E-02	AU116913.1	EST_HUMAN	AU116913 HEMBA1 Homo sapiens cDNA clone HEMBA1000264 5'
469	10412	20231	1.23	7.4E-02	AW838547.1	EST_HUMAN	RC5-LT0054-260100-011-H09 LT0054 Homo sapiens cDNA
1444	11349		1.08	7.4E-02	AF030027.1	NT	Equine herpesvirus 4 strain NS80567, complete genome
2536	12410		0.93	7.4E-02	6755069	NT	Mus musculus paired-like homeodomain transcription factor 1 (Pitx1), mRNA
3545	13461	23255	0.89	7.4E-02	AJ807885.1	EST_HUMAN	wf43h01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2358385 3'
4606	14494	24282	3.38	7.4E-02	L78810.1	NT	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds
4687	14573	24370	2.66	7.4E-02	6978442	NT	Rattus norvegicus Activin receptor like kinase 1 (Acvr1), mRNA
4868	14738	24518	1.7	7.4E-02	6678492	NT	Mus musculus ubiquitin c-terminal hydrolase related polypeptide (Uchrp), mRNA
5913	15819		1.75	7.4E-02	R17477.1	EST_HUMAN	yg14g06.r1 Soares infant brain INIB Homo sapiens cDNA clone IMAGE:32339 5'
6612	16492	26678	1.4	7.4E-02	BE880112.1	EST_HUMAN	601493366F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3895264 5'
6950	16828	27021	1.37	7.4E-02	U66089.1	NT	Human peridolic tryptophan protein 2 (PWP2) gene, exons 15 to 21, and complete cds
9271	18975		2.08	7.4E-02	11525893	NT	Homo sapiens histone deacetylase 5 (NY-CO-9), mRNA
9527	19674		2.82	7.4E-02	AW379431.1	EST_HUMAN	CM4-HT0243-081199-037-d11 HT0243 Homo sapiens cDNA
9678	19235	25242	1.81	7.4E-02	BF035099.1	EST_HUMAN	601453813F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3857738 5'
461	10405	20222	0.96	7.3E-02	BE964961.2	EST_HUMAN	601658738F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886209 3'

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
461	10405	20223	0.96	7.3E-02	BE964961.2	EST_HUMAN	601658738R1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886209 3'
669	10603	20420	2.73	7.3E-02	AE001789.1	NT	Thermoboga maritima section 101 of 136 of the complete genome
1465	12695	21237	3.04	7.3E-02	AW900281.1	EST_HUMAN	CVO-NN1004-130300-284-g08 NN1004 Homo sapiens cDNA
1801	12705		14.81	7.3E-02	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
4927	14806		1.01	7.3E-02	U12283.1	NT	Mus musculus transcription factor USF2 (USF2) gene, exons 8-10 and complete cds
6413	16275	26437	2.44	7.3E-02	P05143	SWISSPROT	PROLINE-RICH PROTEIN MP-3
6413	16275	26438	2.44	7.3E-02	P05143	SWISSPROT	PROLINE-RICH PROTEIN MP-3
6749	16628		1.27	7.3E-02	7662107	NT	Homo sapiens KIAA0424 protein (KIAA0424), mRNA
8548	15788	25910	2.78	7.3E-02	AA779977.1	EST_HUMAN	224402.s1 Soares_fetal_liver_spleen_1NLS_S1 Homo sapiens cDNA clone IMAGE:451178 3' similar to gb:U2426 26S PROTEASE SUBUNIT 4 (HUMAN);
114	10093	19911	0.94	7.2E-02	AE000882.1	NT	Methanobacterium thermoautotrophicum from bases 1029155 to 1039934 (section 88 of 148) of the complete genome
114	10093	19912	0.94	7.2E-02	AE000882.1	NT	Methanobacterium thermoautotrophicum from bases 1029155 to 1039934 (section 88 of 148) of the complete genome
1460	11365	21228	2.23	7.2E-02	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
1460	11365	21229	2.23	7.2E-02	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
2502	12377		2.5	7.2E-02	U14794.1	NT	Human immunodeficiency virus type 1 isolate 26 reverse transcriptase (pol) gene, internal fragment, partial . cds
3810	13722	23511	0.82	7.2E-02	AW298322.1	EST_HUMAN	U1-H-BWO-ajl-a-05-0-U1.s1 NCI_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2732049 3'
4249	14148	23922	4.02	7.2E-02	BF572307.1	EST_HUMAN	602077757F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4251950 5'
4594	14482	24268	78.82	7.2E-02	11466563	NT	Rhodomonas salina mitochondrion, complete genome
4997	14872	24636	0.94	7.2E-02	AB001552.1	NT	Streptococcus mutans gene for glucose-1-phosphate uridylyltransferase, complete cds
5230	15154	24922	3.03	7.2E-02	U67531.1	NT	Methanococcus jannaschii section 73 of 150 of the complete genome
5231	15155	24923	7.62	7.2E-02	P11120	SWISSPROT	CALMODULIN
6282	16118	26272	9.33	7.2E-02	BF216086.1	EST_HUMAN	601883558F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4095710 5'
6281	16145		1.75	7.2E-02	5834897	NT	Strongylocentrotus purpuratus mitochondrion, complete genome
7546	17396	27608	2.05	7.2E-02	AV712452.1	EST_HUMAN	AV712452 DCA Homo sapiens cDNA clone DCAUUG01 5'
7625	17476	27697	4.23	7.2E-02	L14561.1	NT	Homo sapiens plasma membrane calcium ATPase isoform 1 (ATP2B1) gene, alternative splice products, partial cds
7746	17596	27818	2.64	7.2E-02	AW873187.1	EST_HUMAN	hq24f11.x1 NCI_CGAP_Adr1 Homo sapiens cDNA clone IMAGE:3120333 3' similar to TR:Q9Z340 Q9Z340 ATYPICAL PKC SPECIFIC BINDING PROTEIN ;
7926	17776	28016	2.05	7.2E-02	U82695.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7983	17833	28073	5.47	7.2E-02	BE565003.1	EST_HUMAN	601343926F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3685951 5'
7994	17844		3.2	7.2E-02	BE539214.1	EST_HUMAN	601065194F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3451559 5'
8285	18164	28407	4.8	7.2E-02	AF049874.1	NT	Rattus norvegicus bHLH transcription factor Mist1 (Mist1) gene, complete cds
9178	18919	25346	1.44	7.2E-02	AA773696.1	EST_HUMAN	af81a04.r1 Soares NIH-MIPu_31 Homo sapiens cDNA clone IMAGE:1048398 5'
9214	18942		3.13	7.2E-02	AJ230796.1	EST_HUMAN	AJ230796 Homo sapiens library (Seranski P) Homo sapiens cDNA clone PS13D5 3'
9273	18977		1.44	7.2E-02	AA584465.1	EST_HUMAN	nc05h08.s1 NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1099839 3'
9332	19013		1.62	7.2E-02	U82828.1	NT	Homo sapiens ataxia telangiectasia (ATM) gene, complete cds
9346	19331		3.89	7.2E-02	AW900962.1	EST_HUMAN	CM4-NN1009-200300-116-c11 NN1009 Homo sapiens cDNA
1862	11758	21633	1.65	7.1E-02	L02290.1	NT	Human immunodeficiency virus type 1 (D9) proviral structural capsid protein (gag) gene, partial cds
2243	12127		0.9	7.1E-02	AE004890.1	NT	Pseudomonas aeruginosa PA01, section 451 of 529 of the complete genome
2247	12131	22028	5.08	7.1E-02	BF208802.1	EST_HUMAN	601872281F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:4092981 5'
9063	18844		4.98	7.1E-02	BE304764.1	EST_HUMAN	601143974F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3051234 5'
517	10459	20270	1.23	7.0E-02	Q07092	SWISSPROT	COLLAGEN ALPHA 1(XVI) CHAIN PRECURSOR
1484	11389		1.46	7.0E-02	X96877.1	NT	Martellia Mitut-1 gene
1725	11626	21495	1.36	7.0E-02	AA056343.1	EST_HUMAN	z68f04.s1 Stratagene colon (#837204) Homo sapiens cDNA clone IMAGE:509569 3'
2994	12922	22715	1.72	7.0E-02	AW138152.1	EST_HUMAN	UI-H-B11-acy-c-07-0-J1.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2716020 3'
3822	13734	23523	1	7.0E-02	AA815438.1	EST_HUMAN	af65a12.s1 Soares_testis_NHT Homo sapiens cDNA clone 1375678 3' similar to gb:K03002 60S
3958	13866	23642	1.24	7.0E-02	BE070294.1	EST_HUMAN	QV4-BT0407-280100-090-e10 BT0407 Homo sapiens cDNA
4047	13949		1.08	7.0E-02	AW792962.1	EST_HUMAN	CM0-UM0001-060300-270-e12 UM0001 Homo sapiens cDNA
4121	14021	23799	1.27	7.0E-02	AF077821.1	NT	Canis familiaris inducible nitric oxide synthase mRNA, complete cds
4846	14727	24510	7.1	7.0E-02	BF381987.1	EST_HUMAN	601816291F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4050071 5'
7259	17136	27329	1.25	7.0E-02	9628113	NT	African swine fever virus, complete genome
7534	17385	27597	1.19	7.0E-02	K02901.1	NT	Rat Ig germline epsilon H-chain gene C-region, 3' end
8679	18567	28850	2.39	7.0E-02	AA724295.1	EST_HUMAN	ah99a05.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1327184 3' similar to gb:U14837
503	10445	20256	5.34	6.9E-02	AL163210.2	NT	TIGHT JUNCTION PROTEIN ZO-1 (HUMAN);
503	10445	20257	5.34	6.9E-02	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
1311	11217		1.31	6.9E-02	4507968	NT	Homo sapiens chromosome 21 segment HS21C010
3724	13636	23421	1.42	6.9E-02	Q06364	SWISSPROT	Homo sapiens regulator of Gz-selective protein signaling (ZGAP1) mRNA, and translated products
3724	13636	23422	1.42	6.9E-02	Q06364	SWISSPROT	26S PROTEASOME REGULATORY SUBUNIT S3 (NUCLEAR ANTIGEN 21D7)
5100	14968		1.05	6.9E-02	AF079906.1	NT	26S PROTEASOME REGULATORY SUBUNIT S3 (NUCLEAR ANTIGEN 21D7)
							Rabies virus isolate b615 glycoprotein gene, partial cds

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6978	18855	27048	1.37	6.9E-02	BE567435.1	EST_HUMAN	601340661F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3683030 5'
6978	18855	27049	1.37	6.9E-02	BE567435.1	EST_HUMAN	601340661F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3683030 5'
9208	18839		3.95	6.9E-02	X74315.1	NT	Xlaevis XFD2 mRNA for fork head protein
9385	19045		1.5	6.9E-02	P44621	SWISSPROT	PROTEIN TRANSPORT PROTEIN HOFCHOMOLOG
9598	19180		2.19	6.9E-02	AF195953.1	NT	Homo sapiens membrane-bound aminopeptidase P (XNPEP2) gene, complete cds
1839	11736	21610	1.11	6.8E-02	AA496759.1	EST_HUMAN	ae30f02.r1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:897339 5' similar to gb:M22382
1839	11736	21611	1.11	6.8E-02	AA496759.1	EST_HUMAN	ae30f02.r1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:897339 5' similar to gb:M22382
1865	11761	21635	3.91	6.8E-02	AF156673.1	NT	MITOCHONDRIAL MATRIX PROTEIN P1 PRECURSOR (HUMAN);
3062	12989	22780	1.23	6.8E-02	AA781996.1	EST_HUMAN	MITOCHONDRIAL MATRIX PROTEIN P1 PRECURSOR (HUMAN);
3062	12989	22781	1.23	6.8E-02	AA781996.1	EST_HUMAN	Homo sapiens putative hepatic transcription factor (WBSR14) gene, complete cds
3062	12989	22782	1.23	6.8E-02	AA781996.1	EST_HUMAN	ai75a06.s1 Soares_testis_NHT Homo sapiens cDNA clone 1376626 3'
4453	14347		0.92	6.8E-02	BE141076.1	EST_HUMAN	ai75a06.s1 Soares_testis_NHT Homo sapiens cDNA clone 1376626 3'
6315	16178	26337	7.71	6.8E-02	AL163268.2	NT	ai75a06.s1 Soares_testis_NHT Homo sapiens cDNA clone 1376626 3'
8822	16701	26894	6.12	6.8E-02	AJ248287.1	NT	MRO-HT0069-071099-001-c06 HT0069 Homo sapiens cDNA
8822	16701	26895	6.12	6.8E-02	AJ248287.1	NT	Homo sapiens chromosome 21 segment HS21C068
9011	19719		1.37	6.8E-02	T03214.1	EST_HUMAN	Pyrococcus abyssi complete genome, segment 5/6
9140	18895		2.98	6.8E-02	AA758014.1	EST_HUMAN	Pyrococcus abyssi complete genome, segment 5/6
9764	19284		2.97	6.8E-02	9910585	NT	FB4A8 Fetal brain, Striatagene Homo sapiens cDNA clone FB4A8 3'end similar to LINE-1
1511	11416		2.17	6.7E-02	AF115536.1	NT	ah67705.s1 Soares_testis_NHT Homo sapiens cDNA clone 1320705 3'
1851	11747	21622	2.5	6.7E-02	AJ220285.1	EST_HUMAN	Mus musculus latent TGF beta binding protein (Tgfb), mRNA
3656	13570	23356	3.52	6.7E-02	P17278	SWISSPROT	Oncorhynchus mykiss TAP1 protein (OnmyTAP1) mRNA, OnmyTAP1*01 allele, complete cds
1326	11233	21089	1.05	6.6E-02	AJ735509.1	EST_HUMAN	qg79a04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1841406 3'
1347	11253	21109	1.5	6.6E-02	AF245116.1	NT	HOMEBOX PROTEIN HOXD4 (CHOX-A)
2133	12021	21918	3.07	6.6E-02	AJ289241.1	NT	SW:LIN1_NYCCO P08548 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG. ;
3133	13058		1.32	6.6E-02	Q13585	SWISSPROT	at12e09.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2354920 3' similar to
3418	13335	23139	8.61	6.6E-02	R64306.1	EST_HUMAN	Drosophila melanogaster cactin mRNA, complete cds
3432	13349	23154	2.19	6.6E-02	7108357	NT	Mus musculus Capn12 gene for calpain 12, exons 1-21, three alternative transcripts
3432	13349	23155	2.19	6.6E-02	7108357	NT	MELATONIN-RELATED RECEPTOR (H9)
3989	13896	23673	1.59	6.6E-02	AF260225.1	NT	y118b10.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:139579 3'
4904	14784	24558	8.4	6.6E-02	Q61703	SWISSPROT	Homo sapiens mesothelin (MSLN), transcript variant 1, mRNA
4904	14784	24559	8.4	6.6E-02	Q61703	SWISSPROT	Homo sapiens mesothelin (MSLN), transcript variant 1, mRNA
							Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
							INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H2 PRECURSOR (ITI HEAVY CHAIN H2)
							INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H2 PRECURSOR (ITI HEAVY CHAIN H2)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5167	15033	24800	1.34	6.6E-02	AF204882.1	NT	Amsacta albitriga nucleopolyhedrovirus AcORF17 homolog gene, complete cds
5190	15053	24817	0.84	6.6E-02	AE004345.1	NT	Vibrio cholerae chromosome II, section 2 of 93 of the complete chromosome
5968	15873	25998	3.09	6.6E-02	X06411.1	NT	P. vulgaris mRNA for chalcone synthase
6209	15969	26105	2.93	6.6E-02	AI243326.1	EST_HUMAN	qh41d01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1847233 3'
6635	16515	26706	1.48	6.6E-02	AF052572.1	NT	Homo sapiens chemokine receptor CXCR4 gene, promoter region and complete cds
7806	17656	27894	1.37	6.6E-02	Y07848.1	NT	Homo sapiens EWS, gar22, rp22 and bam22 genes
8330	18207	28457	6.28	6.6E-02	BF374248.1	EST_HUMAN	MR1-SN0064-010600-006-a12 SN0064 Homo sapiens cDNA
9593	19175		2.08	6.6E-02	9937991	NT	Mus musculus DIPB gene (Dipb), mRNA
9882	19366		1.46	6.6E-02	AF167430.1	NT	Rattus norvegicus cytochrome P450 2E1 (CYP2E1) gene, 5' flanking region
567	10506	20313	1.91	6.5E-02	BF027639.1	EST_HUMAN	601671046F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3954178 5'
971	10895	20743	1.75	6.5E-02	7708068	NT	Homo sapiens E2F-like protein (LOC51270), mRNA
1369	11275	21131	4.17	6.5E-02	U47624.1	NT	Xenopus laevis alpha(E)-catenin mRNA, complete cds
1702	11603	21474	2.16	6.5E-02	AE000764.1	NT	Aquifex aeolicus section 96 of 109 of the complete genome
5413	15333	25383	1.76	6.5E-02	AA443991.1	EST_HUMAN	zv46h12.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:756743 3' similar to gb:M26038
8035	17927	28173	5.61	6.5E-02	AA195648.1	EST_HUMAN	HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DR-5 BETA CHAIN (HUMAN);
9034	18823		3.53	6.5E-02	M21496.1	NT	z32g05.s1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:665144 3'
9393	19051		3.73	6.5E-02	AF102993.1	NT	Rabbit microsomal epoxide hydrolase
561	10501	20307	1.53	6.4E-02	X94549.1	NT	Nectria haematococca kinesin related protein 2 (KRP2) gene, complete cds
4802	12909	22708	1.35	6.4E-02	6996923	NT	A. carterae precursor of peridinin-chlorophylla-protein (PCP) gene
5180	15044		8.78	6.4E-02	6996923	NT	Mus musculus histone deacetylase 5 (Hdac5), mRNA
5346	15267	25094	1.4	6.4E-02	AI191956.1	EST_HUMAN	q607b01.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1738249 3' similar to contains LTR8.b3
5718	15625	25727	7.58	6.4E-02	AF052733.1	NT	LTR8 repetitive element ;
5718	15625	25728	7.58	6.4E-02	AF052733.1	NT	Heterodera glycines beta-1,4-endoglucanase-1 precursor (HG-eng-1) gene, complete cds
6079	16062	26210	5.23	6.4E-02	BE974448.1	EST_HUMAN	Heterodera glycines beta-1,4-endoglucanase-1 precursor (HG-eng-1) gene, complete cds
6853	16732		2.57	6.4E-02	6753323	NT	601680425R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950503 3'
7034	16911	27099	4.12	6.4E-02	AA093305.1	EST_HUMAN	Mus musculus chaperonin subunit 6a (zeta) (Cct6a), mRNA
7603	17454	27668	2.02	6.4E-02	AB011126.1	NT	k1419.seq.F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA 5'
							Homo sapiens mRNA for KIAA0554 protein, partial cds
8946	18754	29049	1.86	6.4E-02	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, Rofet gene, and sodium phosphate transporter (NPT3) gene, complete cds

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Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8946	18754	29050	1.86	6.4E-02	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NP T3) gene, complete cds
9289	19635		3.65	6.4E-02	AF107890.1	NT	Homo sapiens mucin 5B (MUC5B) gene, partial cds
9337	19017	25295	2.27	6.4E-02	AJ277174.1	NT	Drosophila melanogaster mRNA for mod(mdg4)51.4 protein
1720	11621	21490	2.43	6.3E-02	AF109905.1	NT	Mus musculus major histocompatibility locus class III regions Hsc70t gene, partial cds; smRNP, G7A, NG23, MutS homolog, CLCP, NG24, NG25, and NG26 genes, complete cds; and unknown genes
3552	13467		2.09	6.3E-02	P37092	SWISSPROT	HEAT SHOCK PROTEIN 70 HOMOLOG
7762	17602	27825	3.14	6.3E-02	AB010162.1	NT	Hepatitis G virus RNA for polyprotein (NS5A region), partial cds, strain: CMR-152
8096	15637	25741	3.29	6.3E-02	BF210736.1	EST_HUMAN	601873316F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4097499 5'
9373	19039		1.49	6.3E-02	P15276	SWISSPROT	TRANSCRIPTIONAL REGULATORY PROTEIN ALGP (ALGINATE REGULATORY PROTEIN ALGR3)
4157	14057	23831	3.37	6.2E-02	AL161572.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 68
4243	14142		1.11	6.2E-02	AF271235.1	NT	Rattus norvegicus differentiation-associated Na-dependent inorganic phosphate cotransporter (DNPI) mRNA, complete cds
4479	14373		5.41	6.2E-02	Q62191	SWISSPROT	52 KD RO PROTEIN (SJOJGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A)) (RO52)
4803	14687		1.22	6.2E-02	AV705701.1	EST_HUMAN	AV705701 ADB Homo sapiens cDNA clone ADBAB03 5'
7459	17319	27525	1.21	6.2E-02	6677898	NT	Mus musculus stromal cell derived factor receptor 2 (Sldr2), mRNA
8655	18544	28827	1.84	6.2E-02	AJ242735.1	NT	Metarhizium anisopliae mRNA for Chymotrypsin (chy1 gene)
9129	19762		3.53	6.2E-02	AE000750.1	NT	Aquifex aeolicus section 82 of 109 of the complete genome
9541	19142	25265	1.98	6.2E-02	BF112039.1	EST_HUMAN	7137h08.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3523815 3' similar to TR:Q9Y4S6 Q9Y4S6 HYPOTHETICAL 30.3 KD PROTEIN. [1];
256	10222	20038	4.53	6.1E-02	D16471.1	NT	Human mRNA, Xq terminal portion
3909	13819		2.65	6.1E-02	U73325.1	NT	Arabidopsis thaliana K+ inward rectifying channel protein (AtKCI1) gene, complete cds
5150	15017	24785	1.01	6.1E-02	AB040897.1	NT	Homo sapiens mRNA for KIAA1464 protein, partial cds
6809	16688	26877	3.46	6.1E-02	X99288.1	NT	H. sapiens mRNA for B-HLH DNA binding protein
8112	18002	28248	5.44	6.1E-02	BE179543.1	EST_HUMAN	IL3-HT0618-110500-136-C06 HT0618 Homo sapiens cDNA
9088	19670		7.17	6.1E-02	X70989.1	NT	S. japonicum mRNA for serine-enzyme
9783	19296		3.6	6.1E-02	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
1241	11148	20997	1.41	6.0E-02	AE001777.1	NT	Thermotoga maritima section 89 of 136 of the complete genome
2641	12508	22399	1.57	6.0E-02	AW98848.1	EST_HUMAN	EST380924 MAGE resequences, MAGJ Homo sapiens cDNA
2745	12607		1.61	6.0E-02	AB031289.1	NT	Mesocricetus corti mitochondrial DNA, NADH dehydrogenase subunit 4, tRNA-Phe, tRNA-Met, ATPase subunit 6, and NADH dehydrogenase subunit 2
2806	10076	19892	1.22	6.0E-02	AA188730.1	EST_HUMAN	zp78c04.1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:626310 5'

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Table 4
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2906	10076	19893	1.22	6.0E-02	AA188730.1	EST_HUMAN	zp78c04.r1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:626310 5'
3191	13116	22921	1.2	6.0E-02	AA372376.1	EST_HUMAN	EST184266 Colon adenocarcinoma IV Homo sapiens cDNA 5' end similar to tissue-specific protein
3191	13116	22922	1.2	6.0E-02	AA372376.1	EST_HUMAN	EST184266 Colon adenocarcinoma IV Homo sapiens cDNA 5' end similar to tissue-specific protein
3583	13497		0.9	6.0E-02	BE964443.2	EST_HUMAN	601658150R1 NIH_MGC_98 Homo sapiens cDNA clone IMAGE:3876060 3'
4893	14773	24551	1.17	6.0E-02	Z67739.2	NT	Streptococcus pneumoniae parC, parE and transposase genes and ORF DNA
5314	15235		3.46	6.0E-02	AW370211.1	EST_HUMAN	RC3-BT0253-011199-013-b04 BT0253 Homo sapiens cDNA
6172	15129	24848	2.86	6.0E-02	5174698	NT	Homo sapiens stimulated trans-acting factor (50 kDa) (STAF50) mRNA
6172	15129	24849	2.86	6.0E-02	5174698	NT	Homo sapiens stimulated trans-acting factor (50 kDa) (STAF50) mRNA
6265	16130	26284	1.97	6.0E-02	BF382349.1	EST_HUMAN	601815274F2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4049226 5'
6524	16383	26562	2.05	6.0E-02	AI204275.1	EST_HUMAN	qf58b08.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1764199 3'
7340	17208	27406	1.19	6.0E-02	AI623167.1	EST_HUMAN	ts78a06.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2237362 3'
7340	17208	27407	1.19	6.0E-02	AI623167.1	EST_HUMAN	ts78a06.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2237362 3'
7411	17278	27486	1.79	6.0E-02	AJ245355.1	NT	Acipenser baeri partial IGLV gene for Immunoglobulin light chain variable region, exons 1-2
7411	17278	27487	1.79	6.0E-02	AJ245355.1	NT	Acipenser baeri partial IGLV gene for Immunoglobulin light chain variable region, exons 1-2
9336	19016	25294	1.95	6.0E-02	11431702	NT	Homo sapiens DNA-dependent protein kinase catalytic subunit-interacting protein 2 (KIP2), mRNA
9715	19256		1.84	6.0E-02	AI809273.1	EST_HUMAN	wf69h03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2360885 3' similar to TR:O60298
229	10198	20011	3.42	5.9E-02	AW934719.1	EST_HUMAN	O60298 KIAA0551 PROTEIN ;
2955	12882	22681	2.59	5.9E-02	AF190269.1	NT	RC1-DT0001-290100-012-e10 DT0001 Homo sapiens cDNA
4770	14655	24443	0.88	5.9E-02	AF006304.1	NT	Mus musculus p53 tumor suppressor gene, exon 10 and 11, partial cds; alternatively spliced
7008	16885	27077	1.87	5.9E-02	9055249	NT	Saccharomyces cerevisiae protein tyrosine phosphatase (PTP3) gene, complete cds
8165	18053		2.72	5.9E-02	6679870	NT	Mus musculus iroquois related homeobox 5 (Drosophila) (Irx5), mRNA
8383	18260	28509	3.15	5.9E-02	11433356	NT	Mus musculus follistatin-like (Fstl), mRNA
8842	18655		1.99	5.9E-02	AJ240733.1	NT	Homo sapiens ninein (LOC51199), mRNA
917	10841		4.35	5.8E-02	D90110.1	NT	Gallus gallus HKC9 telomere junction
2830	12759		1.1	5.8E-02	AJ223621.1	NT	Thiobacillus ferrooxidans merC, merA genes and URF-1
3613	13527	29314	1.44	5.8E-02	AE001775.1	NT	Populus trichocarpa COCAOMT1 gene, exon 1 to exon 5
4257	14156	23931	4.36	5.8E-02	AW051927.1	EST_HUMAN	Thermoboga maritima section 87 of 136 of the complete genome
4257	14156	23932	4.36	5.8E-02	AW051927.1	EST_HUMAN	wx24c02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2544578 3'
4447	14341	24132	4.21	5.8E-02	AI247505.1	EST_HUMAN	wx24c02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2544578 3'
4447	14341	24133	4.21	5.8E-02	AI247505.1	EST_HUMAN	qh56f01.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1848697 3' similar to gb:M13142 COAGULATION FACTOR XI PRECURSOR (HUMAN);
4471	14365		2.04	5.8E-02	AF096264.1	NT	qh56f01.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1848697 3' similar to gb:M13142 COAGULATION FACTOR XI PRECURSOR (HUMAN);